

```

ID AAH75831 standard; DNA; 20 BP.
XX
AC AAH75831;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human C2 domains protein, BioHC2, coding sequence PCR primer #2.
XX
KW Human; C2 domain protein; BioHC2; membrane protein; PCR primer;
KW transmembrane transport disorder; ss.
XX
OS Homo sapiens.
XX
DN CN1296954-A.
XX
PD 30-MAY-2001.
XX
PF 19-NOV-1999; 99CN-00124028.
XX
PR 19-NOV-1999; 99CN-00124028.
XX
PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-489555/54.
XX
PT Human membrane protein containing C2 structural domain and its coding
PT sequence.
XX
PS Example 3; Page 12 (Disclosure); 26pp; Chinese.
XX
CC The present invention relates to human C2 domains protein, BioHC2 and
CC coding sequence (see AAH75829 and AAG66417). BioHC2 is a membrane
CC protein, which contains C2 structural domains. BioHC2 and its coding
CC sequence are useful for treating transmembrane transport disorders. The
CC present sequence is a PCR primer, which was used in an example from the
CC present invention
XX
SQ Sequence 20 BP; 5 A; 1 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AAAGATTATTTT 435
DB 5 AAAGATTATTTT 16

RESULT 269
AAF23187
ID AAF23187 standard; DNA; 20 BP.
XX
AC AAF23187;
XX
DT 19-MAR-2001 (first entry)
XX
DE Oligonucleotide for detection of Mycobacterium vaccae.
XX
KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW Mycobacterium flavesens; Mycobacterium asiaticum; tuberculosis;
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
XX
OS Mycobacterium vaccae.
XX
PN WO200073436-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000WO-KR000477.

XX
PR 29-MAY-1999; 99KR-00019631.
PR 29-MAY-1999; 99KR-00019632.
PR 29-MAY-1999; 99KR-00019633.
PR 29-MAY-1999; 99KR-00019634.
PR 29-MAY-1999; 99KR-00019635.
PR 07-APR-2000; 2000KR-00018189.
XX
PA (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
PI Kim CM, Park HK, Jang HJ;
XX
DR WPI; 2001-061527/07.
XX
PT Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
PS Claim 16; Page 45; 89pp; English.
XX
CC The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavesens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridization probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
SQ Sequence 20 BP; 1 A; 3 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGCGGTG 76
DB 5 AGGTCGCGGTG 16

RESULT 270
AAS22314
ID AAS22314 standard; DNA; 20 BP.
XX
AC AAS22314;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human COL9A2 PCR primer 1 for Exon 17.
XX
KW Human; collagen; COL1A1; COL1A2; COL9A1; COL9A2; COL9A3; ss;
KW osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;
KW shortness of stature; low bone density; gene therapy; PCR primer.
XX
OS Homo sapiens.
XX
PN US6285157-B1.
XX
PD 24-JUL-2001.
XX
PF 03-OCT-1997; 97US-00943731.

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XX 03-DEC-1991; 91US-00803628.
PR 13-MAR-1994; 94US-00212322.
XX
XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
XX
XX Prockop DJ, Spotila LD, Deltas CD, Sereda L;
PI Westerhausen Larson A, Pack M, Collige A, Early J, Koerkhoe J;
PI Ala-Kokko L, Annunen S, Pihlajamaa T, Vuoristo M, Paasilta P;
XX
XX WPI; 2001-432201/46.
DR
XX
XX Detecting collagen gene alteration, useful for diagnosing osteoporosis,
PT multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of
PT stature and low bone density in humans.
XX
XX Claim 8; Fig 24; 617pp; English.
XX
XX The invention relates to detecting a collagen gene alteration associated
CC with a pathological condition in a human subject by obtaining from the
CC subject a sample nucleic acid containing a portion of at least 15
CC consecutive nucleotides of the segment of the COL1A1 gene extending in
CC the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent
CC exon 28 through the 3' end of intron 51, where the portion contains an
CC intronic nucleotide and a first and second site, determining the sequence
CC of the portion and comparing the sequence of the portion with the
CC corresponding consensus sequence of the COL1A1 gene where a difference
CC between the sequence of the portion and the consensus sequence indicates
CC the presence of the collagen alteration in the subject. The method is
CC used for detecting abnormalities in a COL1 or COL9 gene is useful for
CC determining whether a subject is afflicted with pathological conditions
CC associated with an altered collagen gene such as osteoporosis, multiple
CC epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and
CC low bone density. Identification of an abnormality in a collagen gene is
CC also useful for designing a therapeutic nucleotide or gene therapy agent
CC which can be administered to the subject to correct or alleviate the
CC abnormality. The method is useful for detecting mutations in both the
CC coding and non-coding sequences of any of the COL1 or COL9 genes.
CC Therefore the method can be used to detect collagen gene alterations
CC which affect either the primary sequence of a collagen protein chain,
CC splicing of the mRNA encoding such chains or regulation of expression of
CC the genes encoding such chains. The present sequence is a PCR primer
CC which amplifies a nucleic acid from a collagen gene of the invention
XX
XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CTGGGACCTTAGA 212
Db 3 CTGGGACCTTAGA 14
|||||
|||||

RESULT 271
ABA94350
ID ABA94350 standard; DNA; 20 BP.
XX
XX ABA94350;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Beta-actin gene fragment amplifying primer Beta ACT-2.
DE
XX
XX Immunostimulant; circularity; angiogenesis; xenotransplantation;
KW metabolic; cytostatic; vulnary; implant; cell growth promoter;
XX JHF gene; beta-actin; PCR primer; ss.
XX
XX Synthetic.
OS
XX

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PN WO200185917-A2.
XX
XX 15-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-GB002056.
XX
XX 10-MAY-2000; 2000US-00568254.
PR 18-JAN-2001; 2001GB-00001315.
PR 26-FEB-2001; 2001US-0271497P.
PR 21-MAR-2001; 2001GB-00007093.
XX
XX (TRIS-) TRISTEM IRELAND LTD.
PA
XX
XX Abuljadayel IMS;
FI
XX WPI; 2002-114181/15.
DR
XX
XX New device for forming and/or increasing the relative number of
PT undifferentiated cells in a cell population (e.g. hematopoietic cells)
PT and for manufacturing a medicament for treating an immunological
PT disorders or cancers.
XX
XX Disclosure; Page 67; 169pp; English.
XX
XX The invention relates to a device for forming and/or increasing the
CC relative number of undifferentiated cells in a cell population including
CC committed cells. The device comprises a means for contacting a more
CC committed cell with a retrodifferentiation means or an agent that causes
CC the more committed cell to retrodifferentiate into an undifferentiated
CC cell. The device is particularly useful for forming and/or increasing the
CC relative number of (a) undifferentiated cells in a cell population
CC including hematopoietic cells; (b) cells having a cell surface marker
CC designation CD34+ and/or HLA-DR+ and/or CD38+ and/or CD117 and/or
CC AC133 and/or CD90 and/or CD45low in a cell population. The
CC retrodifferentiating means of the device is useful for displacing the
CC ratio of normal differentiated cells in a cell population to effect
CC retrodifferentiation of one or more of the differentiated cells to an
CC undifferentiated cell(s). The device and the recomitted cells may be
CC used to manufacture a medicament for treating an immunological disorder
CC or disease. The medicament is useful for treating cancer, autoimmune
CC diseases, blood disorders, cellular or tissue regeneration, organ
CC regeneration, organ or tissue transplants, or congenital metabolic
CC disorders. In particular, device for preparing a stem cell from a more
CC differentiated cell. The stem cells produced are used to repopulate
CC specific cell populations in a patient, such as a haematopoietic cell
CC population or a subpopulation of it, such as CD4 T-lymphocytes and may
CC also be used to heal and reconstitute specialized cell tissue and organs.
CC Sequences ABA94349-350 represents PCR primers for amplifying a fragment
CC of the beta-actin gene
XX
XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
Db 5 TGAGGATCTTCA 16
|||||
|||||

RESULT 272
ABK52018
ID ABK52018 standard; DNA; 20 BP.
XX
XX AC
XX ABK52018;
XX
XX 13-AUG-2002 (first entry)
DT
XX Lambda g11 insert PCR primer Fil.
XX
XX cDNA library; cloning; human disease gene; plant; animal; primer;
KW identification; food production; lambda g11 insert; PCR; ss.
XX

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XX OS Bacteriophage lambda.
XX FN US6372436-B1.
XX PD 16-APR-2002.
XX XX
XX PF 14-SEP-2000; 2000US-00662235.
XX XX
XX PR 14-SEP-2000; 2000US-00662235.
XX XX
XX PA (UMOR ) UNIV MISSOURI.
XX XX
XX PI Pouzyrev AT, Riddle DL;
XX XX
XX DR WPI; 2002-433676/46.
XX XX
XX PT Producing a cDNA library enriched for rare cDNAs and reduced in abundant
XX PT cDNAs to accelerate the identification and cloning of human disease
XX PT genes.
XX PS Claim 14; Col 32; 24pp; English.
XX CC The present invention relates to a new method of producing a cDNA library
XX CC enriched for rare cDNAs and reduced in abundant cDNAs. The method of the
XX CC invention is useful for providing an abundant cDNA pool to create a cDNA
XX CC library with increased representation of rare clones which may expedite
XX CC the identification and cloning of human disease genes. The invention is
XX CC also useful in the cloning of plant or animal genes of importance to food
XX CC production. The method is simple and eliminates steps for in vitro
XX CC transcription and avoids the use of quenching oligonucleotides to prevent
XX CC hybridisation between common sequences in the vector. The present nucleic
XX CC acid sequence represents lambda gt11 insert PCR primer F11 that was used
XX CC in the methods of the invention for library construction and phage DNA
XX CC preparation
XX SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
    Query Match 2.0%; Score 12; DB 6; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.2e+05;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 1 CTCCTGGAGCCC 12
RESULT 273
ABN79607/c
ID ABN79607 standard; DNA; 20 BP.
XX AC ABN79607;
XX XX
XX DT 29-JUL-2002 (first entry)
XX DE Human Fas chimeric phosphorothioate oligonucleotide #19.
XX KW Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;
XX KW vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.
XX OS Homo sapiens.
XX PN US2002004490-A1.
XX PD 10-JAN-2002.
XX XX
XX PF 09-MAR-2001; 2001US-00802669.
XX XX
XX PR 12-APR-1999; 99US-00290640.
XX PR 18-SEP-2000; 2000US-00665615.
XX XX
XX PA (DEAN/) DEAN N M.
XX PA (MARC/) MARCUSON E G.

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PA (WYAT/) WYATT J.
XX (ZHAN/) ZHANG H.
XX Dean NM, Marcusson EG, Wyatt J, Zhang H;
XX WPI; 2002-204886/26.
XX XX
XX PT Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand,
XX PT Fas ligand or Fas associated protein-1 is useful for inhibiting expression of
XX PT Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating
XX PT hepatitis.
XX PS Claim 3; Page 13; 84pp; English.
XX CC This invention relates to an antisense compound encoding Fas, Fas ligand,
XX CC or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated
XX CC signalling is thought to be immunosuppressive, antiinflammatory,
XX CC hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were
XX CC designed to target human Fas. Oligonucleotides were synthesised as
XX CC chimeric oligonucleotides and are useful for treating an animal having an
XX CC autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition
XX CC associated with apoptosis, allograft rejection, or ischemia reperfusion
XX CC injury. Optionally, the above mentioned conditions are prevented by
XX CC contacting the allograft with the antisense oligonucleotide. The
XX CC oligonucleotides are used in diagnostics, therapeutics, prophylaxis and
XX CC as research reagents and in kits. The oligonucleotides are also useful
XX CC for research purposes. The present nucleotide sequence is related to
XX CC human Fas
XX SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
    Query Match 2.0%; Score 12; DB 6; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.2e+05;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 171 GGAATTGCTCTT 182
Db 20 GGAATTGCTCTT 9
RESULT 274
ABL43643/c
ID ABL43643 standard; DNA; 20 BP.
XX AC ABL43643;
XX XX
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:687.
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2001321190-A.
XX PD 20-NOV-2001.
XX XX
XX PF 12-MAR-2001; 2001JP-00068285.
XX PR 10-MAR-2000; 2000JP-00066716.
XX XX
XX PA (RIKA ) RIKAGAKU KENKYUSHO.
XX PA (GENO-) GENOTEX YG.
XX XX
XX DR WPI; 2002-144136/19.
XX XX
XX PT Arraying genome clones.
XX PS Claim 4; Page 18; 528pp; Japanese.
XX CC The present invention describes a method of arraying genome clones. The

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method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCTGTG 349  
| | | | | | | | | |  
Db 12 TCTACTTCTGTG 1

RESULT 275  
ABL44379  
ID ABL44379 standard; DNA; 20 BP.  
AC ABL44379;  
XX  
XX 11-APR-2002 (first entry)  
XX  
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1423.  
XX  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
XX PCR primer; ss.  
XX Homo sapiens.  
XX JP2001321190-A.  
XX 20-NOV-2001.  
XX  
XX 12-MAR-2001; 2001JP-00068285.  
XX  
XX 10-MAR-2000; 2000JP-00066716.  
XX  
XX (RIKA) RIKAGAKU KENKYUSHO.  
XX (GENO-) GENOTEX YG.  
XX  
XX WPI; 2002-144136/19.  
XX  
XX Arraying genome clones.  
XX  
XX Claim 4; Page 32; 528pp; Japanese.

The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to

the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 TGCATGAAATTT 505  
| | | | | | | | | |  
Db 8 TGCATGAAATTT 19

RESULT 276  
AAL47225  
ID AAL47225 standard; DNA; 20 BP.  
XX  
AC AAL47225;  
XX  
XX 22-AUG-2002 (first entry)  
XX  
XX Single-stranded nucleic acid synthesis method related outer primer #3.  
XX  
XX Single-stranded nucleic acid synthesis; strand displacement polymerase;  
XX restriction site; probe; hybridisation assay; PCR; primer; ss.  
XX Unidentified.  
XX WO200234907-A1.  
XX  
XX 02-MAY-2002.  
XX  
XX 26-OCT-2001; 2001WO-JP009452.  
XX  
XX 27-OCT-2000; 2000JP-00328219.  
XX  
XX (EIKE) EIKEN KAGAKU KK.  
XX Nagamine K, Hase T, Notomi T;  
XX  
XX WPI; 2002-417131/44.

Synthesizing one of the sense and antisense strands of double-stranded nucleic acid by cleaving recognition sites in the 5' side, annealing single-stranded regions of DNA before synthesis from 3'-end of the primer.

Example 6; Page 47; 50pp; Japanese.

The present invention relates to a method for synthesising a single-stranded nucleic acid, involving cleaving a double-stranded DNA having a restriction enzyme recognition sequence in the 5' side of a target sequence, annealing and synthesis of a nucleic acid starting from the 3'-end of the primer with a strand displacement polymerase. The method is applicable in the selective synthesis of a single-stranded nucleic acid, particularly one of the sense and antisense strands of double-stranded nucleic acid, for use as e.g. probes for hybridisation assay. The present invention is a PCR primer described in the exemplification of the

Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 AGGATCTTCCAC 330  
 |||||  
 DB 7 AGGATCTTCCAC 18

RESULT 277  
 ABK14334  
 ID ABK14334 standard; DNA; 20 BP.  
 AC  
 AC ABK14334;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Human interleukin-2 antisense PCR primer.  
 XX  
 KW Human; ss; PCR; primer; interleukin-2; neuroprotective; nootropic;  
 KW anticonvulsant; cerebroprotective; antiparkinsonian; vulnerary;  
 KW immunosuppressive; microglia cell line; autoimmune disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; amyotrophic lateral sclerosis; stroke;  
 KW spinal cord injury; ataxia; brain trauma; multiple sclerosis;  
 KW acquired immunodeficiency syndrome; AIDS-dementia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200204604-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 09-JUL-2001; 2001WO-IB001770.  
 XX  
 PR 10-JUL-2000; 2000WO-US018777.  
 PR 15-MAY-2001; 2001US-00855468.  
 PR 22-JUN-2001; 2001US-00887145.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Kim SU;  
 XX  
 PS WPI; 2002-148175/19.  
 XX  
 PT Genetically modified human microglia cell for treating neurodegenerative  
 PT disease, comprises demonstrable phagocytic properties, produces progeny  
 PT in culture, presents surface antigens, and contains modified human  
 PT genomic DNA.  
 XX  
 PS Example; Page 22; 46pp; English.  
 XX  
 CC The invention relates to a genetically modified human microglia cell  
 CC maintained stably in vitro which has (i) has demonstrable phagocytic  
 CC properties; (ii) produces progeny continuously in culture; (iii) presents  
 CC CD11b and CD68 as surface antigens; and (iv) contains human genomic DNA  
 CC that has been genetically modified to include a viral vector carrying at  
 CC least one DNA segment encoding an exogenous gene for intracellular  
 CC expression. The microglia cell line is useful for screening compounds for  
 CC the treatment of autoimmune disease, and is used in the treatment of a  
 CC neurodegenerative disorder e.g. Alzheimer's disease, Parkinson's disease,  
 CC Huntington's disease, amyotrophic lateral sclerosis, stroke, spinal cord  
 CC injuries, ataxia, brain trauma, multiple sclerosis and AIDS-(acquired  
 CC immunodeficiency syndrome)-dementia. The cell line is also useful for  
 CC isolating neurotoxic or neurotrophic molecules naturally produced by  
 CC human microglia. The present sequence is an RT-PCR (reverse transcriptase  
 CC PCR) primer which amplifies a segment of the mRNA for an expressed marker  
 CC gene, used to characterise the cell line  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 434 TTTACTGCTGGA 445  
 |||||  
 DB 9 TTTACTGCTGGA 20

RESULT 278  
 ABI97083/C  
 ID ABI97083 standard; DNA; 20 BP.  
 XX  
 AC ABI97083;  
 XX  
 DT 16-FEB-2002 (first entry)  
 XX  
 DE Capture oligonucleotide Zip ID#4170 oligo #9.  
 XX  
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
 KW oncogene; tumour suppressor; human papillomavirus; forensic;  
 KW environmental monitoring; food industry; feed industry; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200179548-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 04-APR-2001; 2001WO-US010958.  
 XX  
 PR 14-APR-2000; 2000US-0197271P.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Barany F, Zhirvi M, Gerry NP, Favis R, Kliman R;  
 XX  
 DR WPI; 2002-034366/04.  
 XX  
 PT Designing capture oligonucleotide probes for use on a support to which  
 PT complementary oligonucleotides hybridize with little mismatch.  
 XX  
 PS Example 5; Fig 29; 300pp; English.  
 XX  
 CC The present invention describes a method (M1) for designing capture  
 CC oligonucleotide probes (I) for use on a support to which complementary  
 CC oligonucleotide probes (II) will hybridize with little mismatch, where  
 CC (I) have melting temperatures within a narrow range. The method is useful  
 CC for detecting infectious diseases caused by bacterial infectious agents  
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
 CC medinensis. The method is also useful for detecting genetic diseases such  
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair, the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. ABI82074 to  
 CC ABI97546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

```
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 584 CTTGGGACTTT 595
Db 20 CTTGGGACTTT 9

RESULT 279
AB193909/C
ID AB193909 standard; DNA; 20 BP.
XX
AC AB193909;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#996 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 GTCGCTGGGCT 63
Db 12 GTCGCTGGGCT 1

RESULT 280
AB193693
ID AB193693 standard; DNA; 20 BP.
XX
AC AB193693;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#780 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 ACTACCTGTC 90  
 |||||  
 Db 9 ACTACCTGTC 20

RESULT 281  
 AB195383/C  
 ID AB195383 standard; DNA; 20 BP.  
 XX  
 AC  
 AB195383;  
 XX  
 DT 16-FEB-2002 (first entry)  
 XX  
 DE Capture oligonucleotide Zip ID#2470 oligo #9.  
 XX  
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
 KW oncogene; tumour suppressor; human papillomavirus; forensic;  
 KW environmental monitoring; food industry; feed industry; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200179548-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 04-APR-2001; 2001WO-US010958.  
 XX  
 PR 14-APR-2000; 2000US-0197271P.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;  
 XX  
 DR WPI; 2002-034366/04.  
 XX  
 PT Designing capture oligonucleotide probes for use on a support to which  
 PT complementary oligonucleotides hybridize with little mismatch.  
 XX  
 PS Example 5; Fig 29; 300pp; English.  
 XX  
 CC The present invention describes a method (M1) for designing capture  
 CC oligonucleotide probes (I) for use on a support to which complementary  
 CC oligonucleotide probes (II) will hybridise with little mismatch, where  
 CC (I) have melting temperatures within a narrow range. The method is useful  
 CC for detecting infectious diseases caused by bacterial infectious agents  
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
 CC medinensis. The method is also useful for detecting genetic diseases such  
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair, the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. AB182074 to  
 CC AB197546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 AAGAACGGCTGC 165  
 |||||  
 Db 19 AAGAACGGCTGC 8

RESULT 282  
 ABK69394  
 ID ABR69394 standard; DNA; 20 BP.  
 XX  
 AC  
 ABK69394;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide #146 for caspase 9 inhibition.  
 XX  
 KW Antisense compound; caspase 9; C9; hyperproliferative disorder; stroke;  
 KW haematopoietic disorder; cholesterol disorder; bone metabolism disorder;  
 KW brain injury; neurodegenerative disease; infection; inflammation; tumour;  
 KW phosphorothioate backbone linkage; 2'-methoxyethyl; 2'-MOE; ss.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate nucleotides, all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
 XX  
 PN WO200222641-A1.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028233.  
 XX  
 PR 11-SEP-2000; 2000US-00659845.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Zhang H, Watt AT;  
 XX  
 DR WPI; 2002-351874/38.  
 XX  
 PT New antisense oligonucleotide which modulates expression of caspase 9,  
 PT useful to treat tumor, inflammation or to prevent infection in humans.  
 XX  
 PS Claim 26; Page 95; 145pp; English.  
 XX  
 CC The present invention relates to a new antisense compound targeted to a  
 CC nucleic acid molecule encoding caspase 9 (C9). The compound specifically  
 CC hybridises with and inhibits the expression of caspase 9. The invention  
 CC also describes an antisense compound that specifically hybridises with an  
 CC 8 nucleotide portion of an active site of the nucleic acid. The invention  
 CC is useful for inhibiting the expression of C9 in cells or tissues and is  
 CC also useful for treating an animal having a disease or condition  
 CC associated with C9 including a hyperproliferative, haematopoietic or  
 CC cholesterol disorder, bone metabolism disorder, stroke, brain injury or  
 CC neurodegenerative disease. The compound is commonly useful as a research  
 CC and diagnostics reagent. It is also useful to distinguish between  
 CC functions of various members of a biological pathway. The invention is  
 CC also be useful prophylactically e.g. to prevent or delay infection,

CC inflammation or tumour formation. The antisense compound of the invention  
 CC is often preferred over native form because of enhanced cellular uptake,  
 CC enhanced affinity for nucleic acid target and increased stability in  
 CC presence of nucleases. The present nucleic acid sequence represents one  
 CC of a collection (ABK69249-ABK69396) of chimeric phosphorothioate  
 CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings. This sequence was  
 CC used in the methods of the invention for inhibition of caspase 9  
 XX  
 SQ Sequence 20 BP; 7 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGGAGGAAGTT 32  
 |||||  
 Db 5 CCGGAGGAAGTT 16

## RESULT 283

ABZ97922  
 ID ABZ97922 standard; DNA; 20 BP.

XX AC ABZ97922;

XX DT 17-OCT-2003 (first entry)

XX DE Human RANTES oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 13164; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 CAAGGCTGAGCC 368  
 |||||  
 Db 7 CAAGGCTGAGCC 18

## RESULT 284

ABZ94049/C  
 ID ABZ94049 standard; DNA; 20 BP.

XX AC ABZ94049;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 9291; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 11 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 431 ATTTTACTGCT 442  
 Db 13 ATTTTACTGCT 2

RESULT 285  
 ABZ92856/c  
 ID ABZ92856 standard; DNA; 20 BP.  
 XX  
 AC ABZ92856;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX Human oligonucleotide sequence.  
 DE  
 DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX WO200285308-A2.  
 PN 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 8098; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 4 A; 1 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 44 TCAAAAATGTCC 55  
 Db 15 TCAAAAATGTCC 4

RESULT 286  
 ABZ89531/c  
 ID ABZ89531 standard; DNA; 20 BP.  
 XX  
 AC ABZ89531;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX Human oligonucleotide sequence.  
 DE  
 DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX WO200285308-A2.  
 PN 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4773; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAATGTC 54  
 |||||  
 Db 14 TTCAAAATGTC 3

## RESULT 287

ABZ90933/c  
 ID ABZ90933 standard; DNA; 20 BP.

XX AC ABZ90933;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 6175; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGGAAGTTTCT 35  
 |||||  
 Db 12 GAGGAAGTTTCT 1

## RESULT 288

ABZ97923  
 ID ABZ97923 standard; DNA; 20 BP.

XX AC ABZ97923;

XX DT 17-OCT-2003 (first entry)

XX DE Human RANTES oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 13165; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels



CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 357 CAAGGCTGACC 368  
 |||||  
 Db 2 CAAGGCTGACC 13

RESULT 289  
 ABZ88197/C  
 ID ABZ88197 standard; DNA; 20 BP.  
 XX  
 AC ABZ88197;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 3439; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 AGCCTCTTGATG 18  
 |||||  
 Db 17 AGCCTCTTGATG 6

RESULT 290  
 ABZ90932/C  
 ID ABZ90932 standard; DNA; 20 BP.  
 XX  
 AC ABZ90932;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 6174; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGGAAGTTTCT 35  
 |||||  
 Db 18 GAGGAAGTTTCT 7

# RESULT 291

ABZ89530/c

ID ABZ89530 standard; DNA; 20 BP.

AC ABZ89530;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4772; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGTC 54  
 |||||  
 Db 20 TTCAAAAATGTC 9

# RESULT 292

ABZ88369

ID ABZ88369 standard; DNA; 20 BP.

AC ABZ88369;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 3611; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 20 BP; 11 A; 4 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 AAAACCATGAAA 469  
 Db 5 AAAACCATGAAA 16  
 |||||

## RESULT 293

AC82966  
 ID ACC82966 standard; DNA; 20 BP.

XX AC

XX AC82966;

DT 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198838.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;  
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; propylaxis;  
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;  
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone; All cytidine residues  
 are 5-methylcytidines"

FT modified\_base 1..5

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified\_base 16..20

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid  
 PT hormone receptor interactor 6, useful for diagnosing or treating  
 PT hyperproliferative disorders, such as cancer.

XX Example 15; Page 78; 111pp; English.

XX The invention relates to antisense compounds targetted to a nucleic acid

CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its  
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and  
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.  
 CC Antisense compounds of the invention are useful for modulating the  
 CC expression of TRIP6 and for treating diseases or conditions associated  
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.  
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.  
 CC to prevent or delay infection, inflammation or tumour formation, as  
 CC research reagents and kits and in distinguishing between functions of  
 CC various members of a biological pathway. They are also useful in antisense  
 CC therapy. The present sequence is an antisense oligo targetted to human  
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 GGAGCCCTGCT 262

Db 4 GGAGCCCTGCT 15

|||||

## RESULT 294

AAL53980

ID AAL53980 standard; DNA; 20 BP.

XX AC

XX AAL53980;

DT 18-FEB-2003 (first entry)

XX Human serotonin 1B receptor gene PCR primer, SEQ ID No 4.

XX Single nucleotide polymorphism; analgesic; variant allele; A-161T;

KW human serotonin 1B receptor gene; addictive disease; neurologic;

KW psychiatric condition; pain reliever; analgesia; PCR; primer; ss.

XX Homo sapiens.

XX US2002142312-A1.

XX 03-OCT-2002.

XX 15-MAY-2001; 2001US-00855991.

XX 15-MAY-2000; 2000US-0204169P.

XX (CIGL/) CIGLER T.

XX (LAFO/) LAFORGE K S.

XX (KREE/) KREEK M J.

XX Cigler T, Laforge KS, Kreek MJ;

XX WPI; 2003-102507/09.

XX Novel isolated variant allele of human serotonin 1B receptor gene useful  
 PT for determining susceptibility to addictive, neurologic or psychiatric  
 PT conditions or diseases in a subject.

XX Example; Page 12; 20pp; English.

XX The invention relates to a novel isolated variant allele of the human  
 CC serotonin 1B receptor gene, comprising a DNA sequence having a variation  
 CC in a sequence of 1749 base pairs defined in the specification, where the  
 CC variation comprises A-161T. The human serotonin 1B receptor gene is  
 CC useful for determining a susceptibility in a subject to at least one  
 CC addictive disease, neurologic or psychiatric condition or disease. The  
 CC addictive disease comprises opioid addiction, cocaine addiction, or  
 CC addiction to other psychostimulants, nicotine addiction, barbiturate or  
 CC sedative hypotonic addiction, anxiolytic addiction, or alcohol addiction.  
 CC The neurologic or psychiatric condition or disease is anxiety,  
 CC depression, pathological aggression, or compulsive gambling. The human

```
CC serotonin 1B receptor gene is also useful for determining a therapeutic
CC amount of pain reliever to administer to the subject in order to induce
CC analgesia. This polynucleotide sequence represents a PCR primer of the
CC human serotonin 1B receptor gene of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 GACCTACCTGTG 89
Db 4 GACCTACCTGTG 15

RESULT 295
ACCTG0919
ID ACC70919 standard; DNA; 20 BP.
XX
AC ACCTG0919;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cytochrome b PCR primer #12.
XX
KW Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003033737-A1.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-JP010640.
XX
PR 17-OCT-2001; 2001JP-00318805.
XX
PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.
XX
FI Tanaka M;
XX
DR WPI; 2003-393541/37.
XX
PT Gene detection method using human mitochondrial DNA to reveal and confirm
PT amino acid substitution advantageous or disadvantageous in prolonged
PT survival of human, useful for diagnosis of Parkinson's disease.
XX
PS Disclosure; Page 7; 35pp; Japanese.
XX
CC The present invention relates to a detection method using human
CC mitochondrial (mt) DNA. The method comprises detecting the replacement of
CC a base accompanying an amino acid substitution in a protein encoded by
CC its base sequence in a human mitochondrial DNA base sequence. The method
CC is useful for diagnosis of Parkinson's disease, and in health checks and
CC assessing risks for other adult diseases. The present sequence is a PCR
CC primer, which was used to illustrate the invention
XX
SQ Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 CCATGAAGAAC 473
Db 2 CCATGAAGAAC 13

RESULT 296
ABZ59472/c
ID ABZ59472 standard; DNA; 20 BP.
XX
```

```
AC ABZ59472;
XX 17-APR-2003 (first entry)
XX
DE Human src-c chimeric phosphorothioate oligonucleotide SEQ ID NO:93.
XX
KW Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
KW antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
KW antisense oligonucleotide; aberrant bone remodeling; breast cancer;
KW hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
KW ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
KW Kaposi's sarcoma; infection; inflammation; tumour formation;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
XX
PN WO200295053-A2.
XX
PD 28-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-US015684.
XX
PR 18-MAY-2001; 2001US-00860473.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett FC, Watt AT;
XX
DR WPI; 2003-120806/11.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
PT useful for diagnosing, treating or preventing diseases associated with
PT the expression of src-c, e.g. cancer or inflammation, and in research
PT applications.
XX
PS Claim 3; Page 90; 137pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
CC coding region, intron region, exon region, stop codon, intron:exon
CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which
CC specifically hybridises with and inhibits the expression of src-c. (I)
CC have cytostatic, antiinflammatory, osteopathic and antibacterial
CC activities, and can be used in antisense therapy and in vaccines. The
CC antisense compounds (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung
CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents a human src-c antisense chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention
XX
SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
```

Query Match 2.0%; Score 12; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCCGACTTT 291  
DB 15 GTGGCCGACTTT 4

RESULT 297  
ABT14121  
ID ABT14121 standard; DNA; 20 BP.  
XX AC  
XX ABT14121;  
DT 18-FEB-2003 (first entry)  
XX DE  
XX Nucleic acid sequence analysis related oligonucleotide #54.  
XX KW  
XX Primary subunit sequence; variation; secondary subunit sequence;  
XX sequence analysis; refractory behaviour; ds.  
XX OS  
XX Unidentified.  
XX WC200279502-A1.  
XX PN  
XX 10-OCT-2002.  
XX PD  
XX 28-MAR-2002; 2002WO-AU000397.  
XX PF  
XX 28-MAR-2001; 2001US-0279238P.  
XX PR  
XX (UYQU ) UNIV QUEENSLAND.  
XX PA  
XX Keith JM, Bryant DE, Adams P;  
XX PI  
XX WPI; 2003-075457/07.  
XX DR  
XX  
XX Analyzing a primary subunit sequence, useful for sequence analysis,  
XX PT comprises analyzing a secondary subunit sequence which varies from a  
XX PT primary subunit sequence by an addition, deletion and/or substitution of  
XX PT a subunit.  
XX  
XX Disclosure; Page 55; 168pp; English.  
XX PS  
XX The invention relates to a novel method for analysing a primary subunit  
XX CC sequence. The novel method comprises analysing the variation in a  
XX CC secondary subunit sequence, which varies from the primary subunit  
XX CC sequence by the addition, deletion and/or substitution of a subunit, to  
XX CC infer information relative to the primary subunit sequence. The method is  
XX CC useful in sequence analysis and for analysing subunit sequences to infer  
XX CC or otherwise obtain information relating to a property, feature or  
XX CC physical parameter of the subunit sequence, such as its sequence  
XX CC information, structure, size or refractory behaviour to the execution of  
XX CC a task. The secondary subunit sequence is used for analysing refractory  
XX CC behaviour of the primary subunit sequence to the execution of a task, and  
XX CC in deriving a set of subsequences for comparison with a set of  
XX CC subsequences derived from the primary subunit sequence to facilitate the  
XX CC deduction of the primary subunit sequence. This polynucleotide sequence  
XX CC represents an oligonucleotide relating to the analysing method of the  
XX CC invention  
XX  
XX Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 GTCCGCTGGGCT 63  
DB 8 GTCCGCTGGGCT 19

RESULT 298  
ACC99647  
ID ACC99647 standard; DNA; 20 BP.  
XX AC  
XX ACC99647;  
DT 02-SEP-2003 (first entry)  
XX DE  
XX Telenc/ICA PCR primer SEQ ID NO:28.  
XX KW  
XX Multiplex real-time quantitative PCR; PCR primer; copy number;  
XX KW Alzheimer's disease; ss.  
XX OS  
XX Synthetic.  
XX WC2003048377-A2.  
XX PN  
XX 12-JUN-2003.  
XX PD  
XX 02-DEC-2002; 2002WO-US038806.  
XX PF  
XX 30-NOV-2001; 2001US-0336095P.  
XX PR  
XX 19-JUL-2002; 2002US-0397475P.  
XX PR  
XX (UYRP ) UNIV ROCHESTER.  
XX PA (THER/) THERIANOS S.  
XX PI  
XX Zhu M, Coleman P;  
XX PI  
XX WPI; 2003-532841/50.  
XX DR  
XX  
XX Determining the relative copy number of a group of target nucleic acid  
XX PT molecules present in a sample by performing a first or second PCR in a  
XX PT PCR mixture and quantifying the number of copies of the second target  
XX PT nucleic acid product.  
XX  
XX Example 1; Fig 8; 118pp; English.  
XX PS  
XX The present invention describes a multiplex real-time quantitative PCR  
XX CC method for determining the relative copy number of a group of target  
XX CC nucleic acid molecules present in a sample. The method comprises: (1)  
XX CC performing a first PCR in a PCR mixture; (2) performing a second PCR in a  
XX CC PCR mixture; and (3) quantifying the number of copies of the second  
XX CC target nucleic acid product present in the sample containing the target  
XX CC nucleic acid molecule. Also described: (1) quantifying the copy number of  
XX CC a group of target nucleic acids in a sample; and (2) determining whether  
XX CC a subject is at risk of acquiring Alzheimer's disease. The method is  
XX CC useful for determining the relative copy number of a group of target  
XX CC nucleic acid molecules present in a sample for determining whether a  
XX CC subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730  
XX CC represent PCR primer used in the exemplification of the present invention  
XX  
XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TAGACCCCTGGCC 220  
DB 5 TAGACCCCTGGCC 16

RESULT 299  
ABT43789/C  
ID ABT43789 standard; DNA; 20 BP.  
XX AC  
XX ABT43789;  
XX 16-OCT-2003 (first entry)  
XX DE  
XX Human PTP5K1a antisense oligonucleotide Seq ID41.  
XX

KW Human; phosphatidylinositol-4-phosphate 5-kinase Ialpa; PIP5K1alpha;  
 KW antiinflammatory; antitumour; cytostatic; gene therapy; tumour;  
 KW antisense oligonucleotide; hyperproliferative disorder;  
 KW inflammatory disorder; infection; inflammation; 2'-methoxyethyl wing;  
 KW 2'-MOE wing; phosphorothioate backbone; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003050309-A1.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 04-DEC-2002; 2002WO-US038615.  
 XX  
 PR 06-DEC-2001; 2001US-00003354.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Freier SM;  
 XX  
 DR WPI; 2003-627257/59.  
 XX  
 PT New antisense compound useful for treating diseases such as  
 PT hyperproliferative or inflammatory disorders, hybridizes and inhibits  
 PT nucleic acid encoding phosphatidylinositol-4-phosphate 5-kinase, I alpha.  
 XX  
 PS Claim 3; Page 82; 117pp; English.  
 XX  
 CC This invention relates to the novel antisense compounds, particularly  
 CC antisense oligonucleotides, for the modulation of phosphatidylinositol-4-  
 CC phosphate 5-kinase Ialpa (PIP5K1a) expression. The oligonucleotides of  
 CC the invention may have antiinflammatory, antitumour or cytostatic  
 CC activities through use in a gene therapy method. As a result the  
 CC antisense oligonucleotides may be of use for the treatment of an animal  
 CC having a disease associated with PIP5K1a such as a hyperproliferative or  
 CC inflammatory disorder through inhibition of PIP5K1a expression. The  
 CC oligonucleotides of the invention may also be used prophylactically to  
 CC prevent or delay infection, inflammation or tumour formation. They may  
 CC also be useful for diagnostics, therapeutics, prevention, as research  
 CC reagents and kits or for distinguishing functions of various members of a  
 CC biological pathway. The present sequence is that of an antisense  
 CC oligonucleotide of the invention. The oligonucleotide is a chimeric  
 CC phosphorothioate oligonucleotide which has five nucleotide 2'-  
 CC methoxyethyl (2'-MOE) wings with a ten nucleotide deoxynucleotide gap.  
 CC The oligonucleotide backbone is phosphorothioate throughout  
 XX  
 SQ Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 ACAGCCTCTTGA 16  
 DB 12 ACAGCCTCTTGA 1  
 RESULT 300  
 ABT44205/c  
 ID ABT44205 standard; DNA; 20 BP.  
 XX  
 AC ABT44205;  
 XX  
 XX 06-NOV-2003 (first entry)  
 DT  
 XX  
 DE Chimeric antisense oligonucleotide ISIS 199201 to inhibit human NOD1.  
 XX  
 KW Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;  
 KW caspase associated recruitment domain 4; programmed cell death; cancer;  
 KW apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;  
 KW viral infection; human; chimeric.

OS Chimeric - Homo sapiens.  
 XX  
 PN WO2003050246-A2.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 04-DEC-2002; 2002WO-US038606.  
 XX  
 PR 05-DEC-2001; 2001US-00006893.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Dobie KW, Roach MP;  
 XX  
 DR WPI; 2003-577293/54.  
 XX  
 PT New compound, comprising a sequence targeted to a nucleic acid encoding  
 PT nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing  
 PT a composition for treating hyperproliferative disease, e.g., cancer.  
 XX  
 PS Example 15; Page 76; 138pp; English.  
 XX  
 CC This invention relates to novel chimeric antisense oligonucleotides that  
 CC specifically hybridize to and inhibit the expression of the nucleotide  
 CC binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4  
 CC (caspase associated recruitment domain 4) is a domain that is involved in  
 CC the elimination of cells via programmed cell death and in the host  
 CC defence against pathogens, i.e. it works to regulate apoptosis. Apoptosis  
 CC is a naturally occurring process, however, if it becomes overstimulated  
 CC it can lead to cell loss and neurodegenerative conditions including  
 CC Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis  
 CC pigmentosa and blood cell disorders. Conversely, insufficient apoptosis  
 CC can contribute to the development of cancer, autoimmune disorders and  
 CC viral infections. The present invention describes antisense  
 CC oligonucleotides that can modulate NOD1 expression (and variants  
 CC thereof), such that these compounds, via gene therapy, can be used to  
 CC treat various human diseases caused by aberrant apoptosis. This  
 CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit  
 CC expression of human NOD1, the aim of the invention. Note that it has two  
 CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a  
 CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate  
 CC throughout  
 XX  
 SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 585 TTGGGACTTTG 596  
 DB 16 TTGGGACTTTG 5  
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 Job time : 376 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:53:48 ; Search time 306 seconds  
(without alignments)  
7135.578 Million cell updates/sec

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Perfect score: 597  
Sequence: 1 atggacagcccttgatgaa.....ttcgactttggactttga 597

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2421054 seqs, 1828716029 residues

Word size : 0  
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Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
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11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.1	2.5	20	15	US-10-349-143-10030
C 2	14.2	2.3	20	12	Sequence 10030, A
C 3	14.2	2.3	20	14	Sequence 337, App
C 4	14.2	2.3	20	14	Sequence 4739, App
C 5	13.2	2.2	17	14	Sequence 103, App
C 6	13.2	2.2	17	14	Sequence 795, App
C 7	13.2	2.2	17	14	Sequence 796, App
C 8	13.2	2.2	17	14	Sequence 797, App
C 9	13.2	2.2	17	14	Sequence 798, App
C 10	13.2	2.2	17	14	Sequence 799, App
C 11	13.2	2.2	17	14	Sequence 2817, App
C 12	13.2	2.2	17	14	Sequence 3379, App
C 13	13.2	2.2	17	15	Sequence 1006, App
C 14	13.2	2.2	17	15	Sequence 103, App
C 15	13.2	2.2	17	15	Sequence 104, App
C 16	13.2	2.2	19	9	US-09-018-125-9

C 16	13	2.2	19	14	US-10-240-046A-84
C 17	13	2.2	19	15	US-10-223-507-4
C 18	13	2.2	20	9	US-09-752-983-41
C 19	13	2.2	20	10	US-09-954-679-61
C 20	13	2.2	20	14	US-10-215-112-9247
C 21	13	2.2	20	14	US-10-215-112-9359
C 22	13	2.2	20	14	US-10-215-112-9583
C 23	13	2.2	20	14	US-10-215-112-9584
C 24	13	2.2	20	14	US-10-215-112-9587
C 25	13	2.2	20	14	US-10-215-112-9752
C 26	13	2.2	20	14	US-10-215-112-9863
C 27	13	2.2	20	14	US-10-215-112-10087
C 28	13	2.2	20	14	US-10-215-112-10088
C 29	13	2.2	20	14	US-10-215-112-10091
C 30	13	2.2	20	15	US-10-005-341-41
C 31	13	2.2	20	15	US-10-154-708-45
C 32	13	2.2	20	15	US-10-154-708-109
C 33	13	2.2	20	15	US-10-177-554-75
C 34	13	2.2	20	16	US-10-210-589-59
C 35	12	2.0	15	9	US-09-767-395-35
C 36	12	2.0	15	14	US-10-203-860-22
C 37	12	2.0	16	9	US-09-881-012-129
C 38	12	2.0	16	15	US-10-629-951-41
C 39	12	2.0	17	9	US-09-866-108-7364
C 40	12	2.0	17	9	US-09-866-108-7365
C 41	12	2.0	17	9	US-09-866-108-7366
C 42	12	2.0	17	9	US-09-866-108-7367
C 43	12	2.0	17	9	US-09-866-108-7368
C 44	12	2.0	17	9	US-09-866-108-7369
C 45	12	2.0	17	9	US-09-420-433-46

## ALIGNMENTS

### RESULT 1

US-10-349-143-10030/c  
; Sequence 10030, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET\_020CP1  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 10030  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20\_bind  
; OTHER INFORMATION: downstream amplification primer 99-8910 for SEQ 216S, in compler  
US-10-349-143-10030

Query Match 2.5%; Score 15; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GAGGAAGTTCTTTA 38  
Db 15 GAGGAAGTTCTTTA 1

```

RESULT 2
US-10-188-186-337
; Sequence 337, Application US/10188186
; Publication No. US20040029789A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-397C
; CURRENT APPLICATION NUMBER: US/10/188,186
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/360814
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/303828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/323380
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/361133
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/304016
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/373881
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/305673
; PRIOR FILING DATE: 2001-07-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: Custom
; SEQ ID NO 337
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-188-186-337

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Query Match      2.3%; Score 14; DB 12; Length 20;
Best Local Similarity 100.0%; Pred.No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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```

RESULT 3
US-10-032-585-4739/c
; Sequence 4739, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4739
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4739

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Query Match      2.3%; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels

Qy      352 GACCGCAAGGCTGA 365
      |||||
Db      14 GACCGCAAGGCTGA 1

```

RESULT 4  
US-10-262-445-103  
; Sequence 103, Application US/10262445  
; Publication No. US20040014058A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsebrook II, John  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Catterton, Elina  
; APPLICANT: Chant, John  
; APPLICANT: Chaudhuri, Amitabha  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Giot, Loic  
; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Mezes, Peter  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ooi, Chean Eng  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei

APPLICATION: ZHONG, HEN  
 TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS  
 TITLE OF INVENTION: THE SAME  
 FILE REFERENCE: 21402-462D  
 CURRENT APPLICATION NUMBER: US/10/262,445  
 CURRENT FILING DATE: 2002-10-01  
 PRIOR APPLICATION NUMBER: 60/327,454  
 PRIOR FILING DATE: 2001-10-05  
 PRIOR APPLICATION NUMBER: 60/327,917  
 PRIOR FILING DATE: 2001-10-09  
 PRIOR APPLICATION NUMBER: 60/328,029  
 PRIOR FILING DATE: 2001-10-09  
 PRIOR APPLICATION NUMBER: 60/328,056  
 PRIOR FILING DATE: 2001-10-09  
 PRIOR APPLICATION NUMBER: 60/328,849  
 PRIOR FILING DATE: 2001-10-12  
 PRIOR APPLICATION NUMBER: 60/329,414  
 PRIOR FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 60/330,142  
 PRIOR FILING DATE: 2001-10-17  
 PRIOR APPLICATION NUMBER: 60/341,058  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: 60/343,629  
 PRIOR FILING DATE: 2001-10-24  
 PRIOR APPLICATION NUMBER: 60/349,575  
 PRIOR FILING DATE: 2001-10-29  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 133  
 SOFTWARE: Curaseqlist version 0.1  
 SEQ ID NO 103  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe  
 US-10-262-445-103

Query Match 2.3%; Score 14; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;



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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 551 ATGAGGTTGATGAC 564
    |||||
Db 1 ATGAGGTTGATGAC 14

RESULT 5
US-10-060-756A-795/c
; Sequence 795, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 795
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-795

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 17 CTGCACCGCGCCG 5

RESULT 6
US-10-060-756A-796/c
; Sequence 796, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 796
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-796

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 17 CTGCACCGCGCCG 5

RESULT 7
US-10-060-756A-797/c
; Sequence 797, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 797
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-797

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 15 CTGCACCGCGCCG 3

RESULT 8
US-10-060-756A-798/c
; Sequence 798, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
```

```
Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 16 CTGCACCGCGCCG 4

RESULT 9
US-10-060-756A-799/c
; Sequence 799, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 799
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-799

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 15 CTGCACCGCGCCG 3

RESULT 10
US-10-060-756A-800/c
; Sequence 800, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
```

;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/327,898  
;; PRIOR FILING DATE: 2001-10-09  
;; NUMBER OF SEQ ID NOS: 4804  
;; SOFTWARE: Acomica Sequence Listing Engine  
;; SEQ ID NO 798  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-756A-798

Query Match 2.2%; Score 13; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCG 397  
|||||  
DB 14 CTGCACCGCGCG 2

RESULT 9  
US-10-060-756A-799/c  
;; Sequence 799, Application US/10060756A  
;; Publication No. US20030046717A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Zhang, Jian  
;; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
;; FILE REFERENCE: PB0177  
;; CURRENT APPLICATION NUMBER: US/10/060,756A  
;; CURRENT FILING DATE: 2002-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/327,898  
;; PRIOR FILING DATE: 2001-10-09  
;; NUMBER OF SEQ ID NOS: 4804  
;; SOFTWARE: Acomica Sequence Listing Engine  
;; SEQ ID NO 799  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-756A-799

Query Match 2.2%; Score 13; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCG 397  
|||||

Db 13 CTGCACCGCGCG 1  
RESULT 10  
US-10-238-700-2817  
;; Sequence 2817, Application US/10238700  
;; Publication No. US20030153521A1  
;; GENERAL INFORMATION:  
;; APPLICANT: McSwiggen, James  
;; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
;; FILE REFERENCE: 400/057 (MEHB01-1158-A)  
;; CURRENT APPLICATION NUMBER: US/10/238,700  
;; CURRENT FILING DATE: 2002-09-18  
;; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
;; PRIOR FILING DATE: 2002-05-29  
;; PRIOR APPLICATION NUMBER: US 60/318,471  
;; PRIOR FILING DATE: 2001-09-10  
;; NUMBER OF SEQ ID NOS: 4666  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 2817  
;; LENGTH: 17  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-10-238-700-2817

Query Match 2.2%; Score 13; DB 14; Length 17;  
Best Local Similarity 92.3%; Pred. No. 1.8e+04;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGCGG 384  
|||||  
DB 3 GGGGCTGCGCGG 15

RESULT 11  
US-10-238-700-3379/c  
;; Sequence 3379, Application US/10238700  
;; Publication No. US20030153521A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
;; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
;; FILE REFERENCE: 400/057 (MEHB01-1158-A)  
;; CURRENT APPLICATION NUMBER: US/10/238,700  
;; CURRENT FILING DATE: 2002-09-18  
;; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
;; PRIOR FILING DATE: 2002-05-29  
;; PRIOR APPLICATION NUMBER: US 60/318,471  
;; PRIOR FILING DATE: 2001-09-10  
;; NUMBER OF SEQ ID NOS: 4666  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 3379  
;; LENGTH: 17  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-10-238-700-3379

Query Match 2.2%; Score 13; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GCAAGGCTGAGCC 368  
|||||  
DB 15 GCAAGGCTGAGCC 3

RESULT 12  
US-10-297-068-1006  
;; Sequence 1006, Application US/10297068  
;; Publication No. US20030228585A1  
;; GENERAL INFORMATION:  
;; APPLICANT: INOKO, Hidetoshi

APPLICANT: KAGIYA, Taeko  
APPLICANT: ICHIHARA, Tatsuo  
APPLICANT: Matsumura, Yoshiyuki  
APPLICANT: MORIYA, Shogo  
APPLICANT: NISHIDA, Michio  
TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES  
FILE REFERENCE: 13140P174  
CURRENT APPLICATION NUMBER: US/10/297,068  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: JP 2000-164798  
PRIOR FILING DATE: 2000-06-01  
NUMBER OF SEQ ID NOS: 1298  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1006  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: capture  
US-10-297-068-1006

Query Match 2.2%; Score 13; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCCACGTGG 172  
|||||  
DB 3 GGCTGCCACGTGG 15

RESULT 13  
US-10-307-005-103/c

Sequence 103, Application US/10307005  
Publication No. US20030236208A1

GENERAL INFORMATION:

APPLICANT: University of Delaware  
APPLICANT: Eric B. Kmiec  
APPLICANT: Howard B. Gamper  
APPLICANT: Michael C. Rice  
APPLICANT: Jungsup Kim

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants  
TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides

FILE REFERENCE: Napro/009 PCT

CURRENT APPLICATION NUMBER: US/10/307,005

CURRENT FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: PCT/US01/17672

PRIOR FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: US 60/208,538

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US 09/818,875

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 2717

SOFTWARE: Friedman macro Napro4

SEQ ID NO 103

LENGTH: 17

TYPE: DNA

ORGANISM: Hordeum vulgare

US-10-307-005-103

Query Match 2.2%; Score 13; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGACCT 82  
|||||  
DB 16 CGCGGTGACCT 4

RESULT 14

US-10-307-005-104

Sequence 104, Application US/10307005

Publication No. US20030236208A1  
GENERAL INFORMATION:  
APPLICANT: University of Delaware  
APPLICANT: Eric B. Kmiec  
APPLICANT: Howard B. Gamper  
APPLICANT: Michael C. Rice  
APPLICANT: Jungsup Kim  
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants  
TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides  
FILE REFERENCE: Napro/009 PCT  
CURRENT APPLICATION NUMBER: US/10/307,005  
CURRENT FILING DATE: 2002-11-26  
PRIOR APPLICATION NUMBER: PCT/US01/17672  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: US 60/208,538  
PRIOR FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: US 60/244,989  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: US 09/818,875  
PRIOR FILING DATE: 2001-03-27  
NUMBER OF SEQ ID NOS: 2717  
SOFTWARE: Friedman macro Napro4  
SEQ ID NO 104  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Hordeum vulgare  
US-10-307-005-104

Query Match 2.2%; Score 13; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGACCT 82  
|||||  
DB 2 CGCGGTGACCT 14

RESULT 15

US-09-018-125-9

Sequence 9, Application US/09018125A

Patent No. US20010007902A1

GENERAL INFORMATION:

APPLICANT: Silverman, Robert H.

APPLICANT: Kondo, Seiji

APPLICANT: Cowell, John K.

APPLICANT: Li, Gulying

APPLICANT: Torrence, Paul F.

TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES

FILE REFERENCE: 8656-022

CURRENT APPLICATION NUMBER: US/09/018,125A

CURRENT FILING DATE: 1999-02-03

EARLIER APPLICATION NUMBER: 60/044,507

EARLIER FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide

US-09-018-125-9

Query Match 2.2%; Score 13; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407  
|||||  
DB 3 CCGGGGTGCAAT 15

```
RESULT 16
US-10-240-046A-84/c
; Sequence 84, Application US/10240046A
; Publication No. US20030190639A1
; GENERAL INFORMATION:
; APPLICANT: HUGOT, JEAN-PIERRE
; APPLICANT: THOMAS, GILLES
; APPLICANT: ZOULALI, MOHAMED
; APPLICANT: LESAGE, SUZANNE
; APPLICANT: CHAMAILLARD, MATHIAS
; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 37991-0009
; CURRENT APPLICATION NUMBER: US/10/240,046A
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: PCT/FR 01/00935
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: FR 00/03832
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-240-046A-84

Query Match      2.2%; Score 13; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TCGCTGGGGCTAA 65
DB 18 TCGCTGGGGCTAA 6

RESULT 17
US-10-223-507-4/c
; Sequence 4, Application US/10223507
; Publication No. US20030207287A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
; CURRENT APPLICATION NUMBER: US/10/223,507
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/495,052
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-223-507-4

Query Match      2.2%; Score 13; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 508 GTTCGCTCTCCA 520
DB 15 GTTCGCTCTCCA 3

RESULT 18
US-09-752-983-41/c
; Sequence 41, Application US/09752983
; Patent No. US20010016575A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,983
; FILING DATE: 02-Jan-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/280,805
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-752-983-41

Query Match      2.2%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376
DB 19 GAGCCCGAGGGGC 7

RESULT 19
US-09-954-679-61
; Sequence 61, Application US/09954679
; Publication No. US20030100522A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIBONUCLEASE L (2',5'-OLIGOISODENYLATE
; TITLE OF INVENTION: SYNTHETASE-DEPENDENT) EXPRESSION
; FILE REFERENCE: RYS-0212
; CURRENT APPLICATION NUMBER: US/09/954,679
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 88
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```

; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-679-61

Query Match      2.2%; Score 13; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 AGTCTGAGGATCT 325
      |||||
Db 1 AGTCTGAGGATCT 13

RESULT 20
US-10-215-112-9247/c
; Sequence 9247, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9247
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9247

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
      |||||
Db 15 AGACCTACCTGTG 3

RESULT 21
US-10-215-112-9359/c
; Sequence 9359, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9359
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9359

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
      |||||
Db 15 AGACCTACCTGTG 3

RESULT 22
US-10-215-112-9583/c
; Sequence 9583, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9583
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9583

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
      |||||
Db 15 AGACCTACCTGTG 3

RESULT 23
US-10-215-112-9584/c
; Sequence 9584, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9584
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9584

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
      |||||
Db 15 AGACCTACCTGTG 3

RESULT 24
US-10-215-112-9587/c
; Sequence 9587, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119

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```
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9587
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9587

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
    |||||
Db 15 AGACCTACCTGTG 3

RESULT 25
US-10-215-112-9752
; Sequence 9752, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9752
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9752

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
    |||||
Db 15 AGACCTACCTGTG 3

RESULT 26
US-10-215-112-9863
; Sequence 9863, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9863
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9863

Query Match      2.2%; Score 13; DB 14; Length 20;

US-10-215-112-9863
; Sequence 9863, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9863
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9863

Query Match      2.2%; Score 13; DB 14; Length 20;

US-10-215-112-10087
; Sequence 10087, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10087
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10087

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
    |||||
Db 6 AGACCTACCTGTG 18

RESULT 27
US-10-215-112-10088
; Sequence 10088, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10088
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10088

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
    |||||
Db 6 AGACCTACCTGTG 18

RESULT 28
US-10-215-112-10089
; Sequence 10089, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10089
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10089

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
    |||||
Db 6 AGACCTACCTGTG 18

RESULT 29
US-10-215-112-10091
; Sequence 10091, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10091

Query Match      2.2%; Score 13; DB 14; Length 20;
```

```
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10091

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
Db 6 AGACCTACCTGTG 18

RESULT 30
US-10-005-344-41/c
; Sequence 41, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Rich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-41

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7

RESULT 31
US-10-154-708-45
; Sequence 45, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109/c
; Sequence 109, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTTTACTGCT 442
Db 5 TATTTTACTGCT 17

RESULT 32
US-10-154-708-109/c
; Sequence 109, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTTTACTGCT 442
Db 16 TATTTTACTGCT 4

RESULT 33
US-10-177-554-75
; Sequence 75, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-75

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 TGGAGCCCTGCT 262
Db 1 TGGAGCCCTGCT 13
```

RESULT 34  
US-10-210-589-59/c  
; Sequence 59, Application US/10210589  
; Publication No. US20040023381A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Kenneth W. Doble  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP2R1A EXPRESSION  
; FILE REFERENCE: PTS-0041  
; CURRENT APPLICATION NUMBER: US/10/210,589  
; CURRENT FILING DATE: 2002-07-30  
; NUMBER OF SEQ ID NOS: 122  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-589-59  
Query Match 2.2%; Score 13; DB 16; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 237 CTGGTTCACCTCC 249  
Db 14 CTGGTTCACCTCC 2  
RESULT 35  
US-09-767-395-35  
; Sequence 35, Application US/09767395  
; Patent No. US2002000421S1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane K  
; Derbyshire, Blaine J  
; McCafferty, John G  
; Vaughan, Tristan J  
; Johnson, Kevin S  
; TITLE OF INVENTION: Labelling and selection of molecules  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/767,395  
; FILING DATE: 23-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/098,244  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/GB97/01835  
; FILING DATE: 08-JUL-1997  
; APPLICATION NUMBER: GB 9614292.2  
; FILING DATE: 08-JUL-1996  
; APPLICATION NUMBER: GB 9624880.2  
; FILING DATE: 29-NOV-1996  
; APPLICATION NUMBER: GB 9712818.5  
; FILING DATE: 18-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough

REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/34800  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-767-395-35  
Query Match 2.0%; Score 12; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14  
RESULT 36  
US-10-203-860-22  
; Sequence 22, Application US/10203860  
; Publication No. US20030108904A1  
; GENERAL INFORMATION:  
; APPLICANT: WAKAMIYA, No. US20030108904A1utaka  
; TITLE OF INVENTION: No. US20030108904A1el Scavenger Receptor  
; FILE REFERENCE: 19036/38693  
; CURRENT APPLICATION NUMBER: US/10/203,860  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 2000-35155  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 2000-309068  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 28  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of a lambda gt11 5' Sequencing Primer.  
US-10-203-860-22  
Query Match 2.0%; Score 12; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14  
RESULT 37  
US-09-881-012-129/c  
; Sequence 129, Application US/09881012  
; Publication No. US20020192655A1  
; GENERAL INFORMATION:  
; APPLICANT: Gims, Edward I.  
; APPLICANT: Egeiland, Janice A.  
; APPLICANT: Paul, Steven M.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Susceptibility and Resistance Genes for  
; TITLE OF INVENTION: Bipolar Affective Disorder  
; FILE REFERENCE: 015280-248100S  
; CURRENT APPLICATION NUMBER: US/09/881,012  
; CURRENT FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US/09/175,158  
; PRIOR FILING DATE: 1998-10-19  
; PRIOR APPLICATION NUMBER: US 60/062,924  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 240



; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 129  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: D4S1564 forward primer  
US-09-881-012-129

Query Match 2.0%; Score 12; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 TTCACTCCTGG 252  
|||  
Db 15 TTCACTCCTGG 4

## RESULT 38

US-10-629-951-41/C  
; Sequence 41, Application US/10629951  
; Publication No. US2004018550A1  
; GENERAL INFORMATION:  
; APPLICANT: Bellacosa, Alfonso  
; TITLE OF INVENTION: Methods for Detection of Transition  
; FILE REFERENCE: FCCC 96-21  
; CURRENT APPLICATION NUMBER: US/10/629,951  
; PRIOR FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: US/09/629,222A  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 09/463,891  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: PCT/US98/15828  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 60/053,936  
; PRIOR FILING DATE: 1997-07-28  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 41  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-629-951-41

Query Match 2.0%; Score 12; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 CTACATCCTTTT 127  
|||  
Db 15 CTACATCCTTTT 4

## RESULT 39

US-09-866-108-7364  
; Sequence 7364, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 7364  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7364

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510  
|||  
Db 6 GAAATTCAGTT 17

## RESULT 40

US-09-866-108-7365  
; Sequence 7365, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 7365  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7365

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e-04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510  
|||||  
Db 5 GAAATTCAGTT 16

## RESULT 41

US-09-866-108-7366  
; Sequence 7366, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: ACOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 7366  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7366

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e-04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510  
|||||  
Db 4 GAAATTCAGTT 15

## RESULT 42

US-09-866-108-7367  
; Sequence 7367, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: ACOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 7367

;  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7367

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510  
|||||  
Db 3 GAAATTCAGTT 14

## RESULT 43

US-09-866-108-7368  
; Sequence 7368, Application US/09866108  
; Patent No. US20020048800A1

## GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 7368  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7368

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510

Db 2 GAAATTCAGTT 13  
|||||

## RESULT 44

US-09-866-108-7369  
; Sequence 7369, Application US/09866108  
; Patent No. US20020048800A1

## GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 7369  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7369

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510

Db 1 GAAATTCAGTT 12  
|||||

## RESULT 45

US-09-420-433-46  
; Sequence 46, Application US/09420433  
; Patent No. US2002009480A1

## GENERAL INFORMATION:

; APPLICANT: Sidransky, David

;; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN  
;; TITLE OF INVENTION: HISTOLOGIC TISSUE  
;; NUMBER OF SEQUENCES: 82  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Spensley Horn Jubas & Lubitz  
;; STREET: 1880 Century Park East, Suite 500  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90067  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/420,433  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/181,664  
;; FILING DATE: JANUARY 14, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wetherell, Jr., Ph.D., John R.  
;; REGISTRATION NUMBER: 31,678  
;; REFERENCE/DOCKET NUMBER: PD-3055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 455-5100  
;; TELEFAX: (619) 455-5110  
;; INFORMATION FOR SEQ ID NO: 46:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..17  
US-09-420-433-46

Query Match 2.0%; Score 12; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGGCTGCATGAA 501  
|||  
Db 5 GGGCTGCATGAA 16

RESULT 46  
US-09-730-289B-166  
; Sequence 166, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MEHB00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 166  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-730-289B-166

Query Match 2.0%; Score 12; DB 10; Length 17;

Best Local Similarity 33.3%; Pred. No. 6.5e+04;  
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;  
Qy 428 ATTATTTTACT 439  
|:|:|:|:|:|:  
Db 6 AUUAUUUUUACU 17

RESULT 47  
US-09-730-289B-167  
; Sequence 167, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MEHB00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 167  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-730-289B-167

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 33.3%; Pred. No. 6.5e+04;  
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 428 ATTATTTTACT 439  
|:|:|:|:|:|:  
Db 4 AUUAUUUUUACU 15

RESULT 48  
US-09-730-289B-168  
; Sequence 168, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MEHB00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 168  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-730-289B-168

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 33.3%; Pred. No. 6.5e+04;  
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 428 ATTATTTTACT 439  
|:|:|:|:|:|:  
Db 3 AUUAUUUUUACU 14

RESULT 49  
US-09-730-289B-169  
; Sequence 169, Application US/09730289B

```

; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: WEH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-169

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches      4; Conservative      8; Mismatches      0; Indels      0; Gaps      0;

Qy      428 ATTATTTTACT 439
Db      2 AUUAUUUUUACU 13

RESULT 50
US-09-730-289B-170
; Sequence 170, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: WEH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-170

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches      4; Conservative      8; Mismatches      0; Indels      0; Gaps      0;

Qy      428 ATTATTTTACT 439
Db      1 AUUAUUUUUACU 12

RESULT 51
US-09-818-875-163
; Sequence 163, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmlec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176

```

; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 191  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-191

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27  
Db 2 ATGAACCGGAGG 13

RESULT 54  
US-09-818-875-192/c  
; Sequence 192, Application US/09818875  
; Publication No. US20030051270A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 192  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-192

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27  
Db 16 ATGAACCGGAGG 5

RESULT 55  
US-09-818-875-191/c  
; Sequence 51, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim

; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 51  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-51

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 CTGAGCCCGAGG 373  
Db 17 CTGAGCCCGAGG 6

RESULT 56  
US-09-780-533A-947/c  
; Sequence 947, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 947  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-947

Query Match 2.0%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 CTGAGCCCGAGG 373  
Db 12 CTGAGCCCGAGG 1

RESULT 57  
US-09-780-533A-1846/c  
; Sequence 1846, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797

```
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1846

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 14 CTGAGCCCGAGG 3

RESULT 58
US-09-780-533A-2420/c
; Sequence 2420, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2420
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2420

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 16 CTGAGCCCGAGG 5

RESULT 59
US-09-780-533A-2421/c
; Sequence 2421, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2421
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-09-780-533A-2421

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 15 CTGAGCCCGAGG 4

RESULT 60
US-10-060-756A-794/c
; Sequence 794, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 794
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-794

Query Match      2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 TGCACCGCGCGG 397
Db 17 TGCACCGCGCGG 6

RESULT 61
US-10-060-756A-800/c
; Sequence 800, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
```

;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/327,898  
;; PRIOR FILING DATE: 2001-10-09  
;; NUMBER OF SEQ ID NOS: 4804  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; SEQ ID NO 800  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-756A-800

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 385 CTGCACCGCGCC 396  
Db 12 CTGCACCGCGCC 1

## RESULT 62

US-10-060-895A-804  
; Sequence 804, Application US/10060895A  
; Publication No. US20030104403A1  
; GENERAL INFORMATION:

;; APPLICANT: Zhang, Jian  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A

;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/315,984  
;; PRIOR FILING DATE: 2001-08-30  
;; NUMBER OF SEQ ID NOS: 1682  
;; SOFTWARE: Aecomica Sequence Listing Engine

;; SEQ ID NO 804  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-895A-804

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 CCACGTGGAATT 176  
Db 6 CCACGTGGAATT 17

## RESULT 63

US-10-060-895A-805  
; Sequence 805, Application US/10060895A  
; Publication No. US20030104403A1  
; GENERAL INFORMATION:

;; APPLICANT: Zhang, Jian  
;; APPLICANT: Gu, Yizhong  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A

;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/315,984  
;; PRIOR FILING DATE: 2001-08-30  
;; NUMBER OF SEQ ID NOS: 1682  
;; SOFTWARE: Aecomica Sequence Listing Engine

;; SEQ ID NO 805  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-895A-805

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 CCACGTGGAATT 176  
Db 5 CCACGTGGAATT 16

## RESULT 64

US-10-060-895A-806  
; Sequence 806, Application US/10060895A  
; Publication No. US20030104403A1  
; GENERAL INFORMATION:

;; APPLICANT: Zhang, Jian  
;; APPLICANT: Gu, Yizhong  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A

;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30



;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/315,984  
;; PRIOR FILING DATE: 2001-08-30  
;; NUMBER OF SEQ ID NOS: 1682  
;; SOFTWARE: Acomica Sequence Listing Engine  
;; SEQ ID NO 806  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-895A-806

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176  
|||||  
DB 4 CCACGTGGAATT 15

RESULT 65  
US-10-060-895A-807  
;; Sequence 807, Application US/10060895A  
;; Publication No. US20030104403A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Zhang, Jian  
;; APPLICANT: Gu, Yizhong  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE 10  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A  
;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/315,984  
;; PRIOR FILING DATE: 2001-08-30  
;; NUMBER OF SEQ ID NOS: 1682  
;; SOFTWARE: Acomica Sequence Listing Engine  
;; SEQ ID NO 807  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-895A-807

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176  
|||||  
DB 3 CCACGTGGAATT 14

RESULT 66  
US-10-060-895A-808  
;; Sequence 808, Application US/10060895A  
;; Publication No. US20030104403A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Zhang, Jian  
;; APPLICANT: Gu, Yizhong  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE 1  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A  
;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/315,984  
;; PRIOR FILING DATE: 2001-08-30  
;; NUMBER OF SEQ ID NOS: 1682  
;; SOFTWARE: Acomica Sequence Listing Engine  
;; SEQ ID NO 808  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-895A-808

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176  
|||||  
DB 2 CCACGTGGAATT 13

RESULT 67  
US-10-060-895A-809  
;; Sequence 809, Application US/10060895A  
;; Publication No. US20030104403A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Zhang, Jian  
;; APPLICANT: Gu, Yizhong  
;; APPLICANT: Nguyen, Cung-Tuong  
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE 1  
;; FILE REFERENCE: PB0158  
;; CURRENT APPLICATION NUMBER: US/10/060,895A  
;; CURRENT FILING DATE: 2002-06-10  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663

```

? APPLICANT: MCSwaggan, James
? TITLE OF INVENTION: Nucleic Acid Treatment
? FILE REFERENCE: 400/057 (MBHB01-1158-A)
? CURRENT APPLICATION NUMBER: US/10/238,700
? CURRENT FILING DATE: 2002-09-18
? PRIOR APPLICATION NUMBER: PCT/US 02/16840
? PRIOR FILING DATE: 2002-05-29
? PRIOR APPLICATION NUMBER: US 60/318,471
? PRIOR FILING DATE: 2001-09-10
? NUMBER OF SEQ ID NOS: 4566
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 3224
? LENGTH: 17
? TYPE: RNA
? ORGANISM: Homo sapiens
US-10-238-700-3224
Query Match 2.0%; Score 12; DB 14; Length 17;

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Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 267 CTGTGCGCGACA 278  
Db 12 CTGTGCGCGACA 1

RESULT 72  
US-10-238-700-3427/c  
; Sequence 3427, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBH01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3427  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-3427

Query Match 2.0%; Score 12; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 303 CCCCAACCTCAG 314  
Db 15 CCCCAACCTCAG 4

RESULT 73  
US-10-209-787-163  
; Sequence 163, Application US/10209787  
; Publication No. US20030217377A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/10/209,787  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 163  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-209-787-163

Query Match 2.0%; Score 12; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGGAGG 27  
Db 15 ATGAACCGGAGG 4

RESULT 74  
US-10-209-787-164/c  
; Sequence 164, Application US/10209787  
; Publication No. US20030217377A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/10/209,787  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 164  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-209-787-164

Query Match 2.0%; Score 12; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGGAGG 27  
Db 15 ATGAACCGGAGG 4

RESULT 75  
US-10-209-787-191  
; Sequence 191, Application US/10209787  
; Publication No. US20030217377A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/10/209,787  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 191

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGGAGG 27  
Db 3 ATGAACCGGAGG 14

RESULT 76  
US-10-209-787-164/c  
; Sequence 164, Application US/10209787  
; Publication No. US20030217377A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/10/209,787  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 164  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-209-787-164

Query Match 2.0%; Score 12; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGGAGG 27  
Db 15 ATGAACCGGAGG 4

RESULT 77  
US-10-209-787-191  
; Sequence 191, Application US/10209787  
; Publication No. US20030217377A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/10/209,787  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 191



```
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 191
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-191

Query Match      2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      2 ATGAACCGGAGG 13

RESULT 80
US-10-261-185-192/c
; Sequence 192, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 192
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-192

Query Match      2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      16 ATGAACCGGAGG 5

RESULT 81
US-09-942-588A-42/c
; Sequence 42, Application US/09942588A
; Patent No. US20020106667A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Screening method for gene variation
; FILE REFERENCE: CFO 15717
; CURRENT APPLICATION NUMBER: US/09/942,588A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263396
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-588A-42

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 82
US-09-942-588A-65
; Sequence 65, Application US/09942588A
; Patent No. US20020106667A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Screening method for gene variation
; FILE REFERENCE: CFO 15717
; CURRENT APPLICATION NUMBER: US/09/942,588A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263396
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: p53 fragment
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-588A-65

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      1 ATGAACCGGAGG 12

RESULT 83
US-09-764-420A-1
; Sequence 1, Application US/09764420A
; Patent No. US20020115072A1
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadaashi
; APPLICANT: Yamamoto, No. US20020115072A1uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
```

```
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-1

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
Db      1 ATGAACCGGAGG 12

RESULT 84
US-09-764-420A-43/c
; Sequence 43, Application US/09764420A
; Patent No. US20020115072A1
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20020115072A1uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-43

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 85
US-09-875-573-8
; Sequence 8, Application US/09875573
; Patent No. US20020150302A1
; GENERAL INFORMATION:
; APPLICANT: Tarr, Phillip I.
; TITLE OF INVENTION: POLYMORPHIC LOCI THAT DIFFERENTIATE
; TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 FROM OTHER STRAINS
; FILE REFERENCE: CHMED.001C1
; CURRENT APPLICATION NUMBER: US/09/875,573
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US99/29149
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/111,493
; PRIOR FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-875-573-8

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      186 CCGCTACATCTC 197
Db      4 CCGCTACATCTC 15

RESULT 86
US-09-942-596A-42/c
; Sequence 42, Application US/09942596A
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Method of analyzing base sequence of nucleic acid
; FILE REFERENCE: CPO 15718
; CURRENT APPLICATION NUMBER: US/09/942,596A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 263506/2000
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-596A-42

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 87
US-09-942-596A-65
; Sequence 65, Application US/09942596A
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Method of analyzing base sequence of nucleic acid
; FILE REFERENCE: CPO 15718
; CURRENT APPLICATION NUMBER: US/09/942,596A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 263506/2000
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: p53 fragment
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-596A-65

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 16 ATGAACCGGAGG 27  
 Db 1 ATGAACCGGAGG 12

## RESULT 88

US-09-988-873A-42/c  
 ; Sequence 42, Application US/09988873A  
 ; Publication No. US20030027160A1  
 ; GENERAL INFORMATION:

; APPLICANT: Canon Inc.  
 ; TITLE OF INVENTION: Terminal labelled probe array and method of making it  
 ; FILE REFERENCE: CF015961  
 ; CURRENT APPLICATION NUMBER: US/09/988,873A  
 ; PRIOR FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: JP2000-357446  
 ; PRIOR FILING DATE: 2000-11-24  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SEQ ID NO 42  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesized  
 US-09-988-873A-42

Query Match 2.0%; Score 12; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27  
 Db 18 ATGAACCGGAGG 7

## RESULT 89

US-09-988-873A-65  
 ; Sequence 65, Application US/09988873A  
 ; Publication No. US20030027160A1  
 ; GENERAL INFORMATION:

; APPLICANT: Canon Inc.  
 ; TITLE OF INVENTION: Terminal labelled probe array and method of making it  
 ; FILE REFERENCE: CF015961  
 ; CURRENT APPLICATION NUMBER: US/09/988,873A  
 ; CURRENT FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: JP2000-357446  
 ; PRIOR FILING DATE: 2000-11-24  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SEQ ID NO 65  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesized  
 US-09-988-873A-65

Query Match 2.0%; Score 12; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27  
 Db 1 ATGAACCGGAGG 12

## RESULT 90

US-09-972-115A-17  
 ; Sequence 17, Application US/09972115A  
 ; Publication No. US20030032769A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gregg, Morin B.

; APPLICANT: Walter, Funk D.  
 ; APPLICANT: Misczyslaw, Piatyszek A.  
 ; TITLE OF INVENTION: A Second Mammalian Telomerase  
 ; FILE REFERENCE: 080/003C  
 ; CURRENT APPLICATION NUMBER: US/09/972,115A  
 ; CURRENT FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,577  
 ; PRIOR FILING DATE: 2000-04-10  
 ; PRIOR APPLICATION NUMBER: US 60/129,123  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 17  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-09-972-115A-17

Query Match 2.0%; Score 12; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGGCC 257  
 Db 3 CTCCTGGAGGCC 14

## RESULT 91

US-09-942-662A-42/c  
 ; Sequence 42, Application US/09942662A  
 ; Publication No. US20030190612A1  
 ; GENERAL INFORMATION:

; APPLICANT: Canon Inc.  
 ; TITLE OF INVENTION: An assay of many samples for multiple items at the same time  
 ; FILE REFERENCE: 3912041  
 ; CURRENT APPLICATION NUMBER: US/09/942,662A  
 ; CURRENT FILING DATE: 2001-08-31  
 ; PRIOR APPLICATION NUMBER: JP 2000-263395  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: JP 2000-263505  
 ; PRIOR FILING DATE: 2000-08-31  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 42  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sample oligonucleotide  
 US-09-942-662A-42

Query Match 2.0%; Score 12; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27  
 Db 18 ATGAACCGGAGG 7

## RESULT 92

US-09-764-420A-1  
 ; Sequence 1, Application US/09764420A  
 ; Publication No. US20030198952A9  
 ; GENERAL INFORMATION:

; APPLICANT: Okamoto, Tadashi  
 ; APPLICANT: Yamamoto, No. US20030198952A9uko  
 ; APPLICANT: Suzuki, Tomohiro  
 ; TITLE OF INVENTION: Probe Bound Substrate, Process For  
 ; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of  
 ; TITLE OF INVENTION: Detecting Target Substance, Method Of  
 ; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-

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; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-1

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 93
US-09-764-420A-43/c
; Sequence 43, Application US/09764420A
; Publication No. US20030198952A9
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20030198952A9uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-43

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 94
US-10-231-302-42/c
; Sequence 42, Application US/10231302
; Publication No. US20030082602A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20030082602A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for analyzing base sequence of nucleic acid
```

```
; FILE REFERENCE: 03500.015203
; CURRENT APPLICATION NUMBER: US/10/231,302
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP00/07244
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-302-42

Query Match      2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      18 ATGAACCGGAGG 7

RESULT 95
US-10-231-302-65
; Sequence 65, Application US/10231302
; Publication No. US20030082602A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20030082602A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for analyzing base sequence of nucleic acid
; FILE REFERENCE: 03500.015203
; CURRENT APPLICATION NUMBER: US/10/231,302
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP00/07244
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-302-65

Query Match      2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 96
US-10-128-463-10
; Sequence 10, Application US/10128463
; Publication No. US20030171314A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Department of Agriculture, Agricultural Research Service
; APPLICANT: Grubman, Marvin J.
; APPLICANT: Chingamaram, Jarasvech
; APPLICANT: Koster, Marla
; APPLICANT: Moraes, Mauro P.
; TITLE OF INVENTION: Foot and Mouth Disease Virus Vaccine
; FILE REFERENCE: D.N. 0128.01
; CURRENT APPLICATION NUMBER: US/10/128,463
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/286,345
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
```



```
; TYPE: DNA
; ORGANISM: Porcine
US-10-128-463-10

Query Match      2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 CCCCAACTCAG 314
Db 5 CCCCAACTCAG 16

RESULT 97
US-10-418-552-128
; Sequence 128, Application US/10418552
; Publication No. US2003023672A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; APPLICANT: VAN BENENNAAM, Alison
; APPLICANT: VENKATRAJESH, Wylavapu
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR REGULATION OF PLANT GAMMA-
; TITLE OF INVENTION: TOCOPHEROL METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029 (S29-US1)
; CURRENT APPLICATION NUMBER: US/10/418,552
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,488
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/385,992
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/442,470
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 128
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cGMT reverse primer
US-10-418-552-128

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGCC 256
Db 6 CCTCCTGGAGCC 17

RESULT 98
US-10-608-804-42/c
; Sequence 42, Application US/10608804
; Publication No. US20040014124A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Tadashi
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Shimizu, Satoshi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for Examining Reactivity and Method for Detecting a Comple
; FILE REFERENCE: 03500.015716.1
; CURRENT APPLICATION NUMBER: US/10/608,804
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US/09/942,662
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263395
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263505
; PRIOR FILING DATE: 2000-08-31
```

```
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-10-608-804-42

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27
Db 18 ATGAACCGGAGG 7

RESULT 99
US-10-634-510-42/c
; Sequence 42, Application US/10634510
; Publication No. US20040018552A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/10/634,510
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-10-634-510-42

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27
Db 18 ATGAACCGGAGG 7

RESULT 100
US-10-634-510-65
; Sequence 65, Application US/10634510
; Publication No. US20040018552A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/10/634,510
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-10-634-510-65

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27
Db 18 ATGAACCGGAGG 7
```

QY 16 ATGACCGGAGG 27  
| | | | | | | | | |  
Db 1 ATGACCGGAGG 12

## RESULT 101

US-10-444-206-293/c  
; Sequence 293, Application US/10444206  
; Publication No. US2004003917A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Clarence Frank  
; APPLICANT: Vickers, Timothy A.  
; APPLICANT: Karas, James G.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/444,206  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: 09/851,871  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: PCT/US00/14471  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 09/326,186  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 08/777,266  
; PRIOR FILING DATE: 1996-12-31  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 293  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-444-206-293

Query Match 2.0%; Score 12; DB 16; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGCGTGAGCC 369  
| | | | | | | | | |  
Db 14 AAGCGTGAGCC 3

## RESULT 102

US-09-805-177-7  
; Sequence 7, Application US/09805177  
; Patent No. US20020001805A1  
; GENERAL INFORMATION:  
; APPLICANT: Richard Bruce Roden  
; APPLICANT: Honami Naora  
; TITLE OF INVENTION: IMMUNOGENIC OVARIAN CANCER GENES  
; FILE REFERENCE: 031787.0090  
; CURRENT APPLICATION NUMBER: US/09/805,177  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,226  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: 60/259,452  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primers  
US-09-805-177-7

Query Match 2.0%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328  
| | | | | | | | | |  
Db 8 TGAGGATCTTCA 19

## RESULT 103

US-09-068-817-7/c  
; Sequence 7, Application US/09068817  
; Patent No. US20020081733A1  
; GENERAL INFORMATION:  
; APPLICANT: Verfaillie, C.M.  
; APPLICANT: McIvor, R.S.  
; APPLICANT: Zhou, R.C.  
; TITLE OF INVENTION: Method to prepare drug-resistant, non-malignant hematopoietic ce  
; FILE REFERENCE: 600.347US2  
; CURRENT APPLICATION NUMBER: US/09/068,817  
; CURRENT FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/US96/18273  
; PRIOR FILING DATE: 1996-11-13  
; PRIOR APPLICATION NUMBER: US 60/006,692  
; PRIOR FILING DATE: 1995-11-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-068-817-7

Query Match 2.0%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328  
| | | | | | | | | |  
Db 19 TGAGGATCTTCA 8

## RESULT 104

US-09-068-817-8/c  
; Sequence 8, Application US/09068817  
; Patent No. US20020081733A1  
; GENERAL INFORMATION:  
; APPLICANT: Verfaillie, C.M.  
; APPLICANT: McIvor, R.S.  
; APPLICANT: Zhou, R.C.  
; TITLE OF INVENTION: Method to prepare drug-resistant, non-malignant hematopoietic ce  
; FILE REFERENCE: 600.347US2  
; CURRENT APPLICATION NUMBER: US/09/068,817  
; CURRENT FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/US96/18273  
; PRIOR FILING DATE: 1996-11-13  
; PRIOR APPLICATION NUMBER: US 60/006,692  
; PRIOR FILING DATE: 1995-11-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-068-817-8

Query Match 2.0%; Score 12; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328  
| | | | | | | | | |  
Db 19 TGAGGATCTTCA 8

## RESULT 105

US-10-224-005-29/c  
 ; Sequence 29, Application US/10224005  
 ; Publication No. US20030143732A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Fossnaugh, Kathy  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD  
 ; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA  
 ; FILE REFERENCE: 900/041 (MEHB01-1110-A)  
 ; CURRENT APPLICATION NUMBER: US/10/224,005  
 ; CURRENT FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: US 60/315,315  
 ; PRIOR FILING DATE: 2001-08-28  
 ; NUMBER OF SEQ ID NOS: 347  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 29  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense 1  
 US-10-224-005-29

Query Match 2.0%; Score 12; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 CCTGGTTACCT 247  
 ||:|||||  
 Db 19 CCTGGTTACCT 8

RESULT 106  
 US-10-224-005-190  
 ; Sequence 190, Application US/10224005  
 ; Publication No. US20030143732A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Fossnaugh, Kathy  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD  
 ; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA  
 ; FILE REFERENCE: 900/041 (MEHB01-1110-A)  
 ; CURRENT APPLICATION NUMBER: US/10/224,005  
 ; CURRENT FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: US 60/315,315  
 ; PRIOR FILING DATE: 2001-08-28  
 ; NUMBER OF SEQ ID NOS: 347  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 190  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
 US-10-224-005-190

Query Match 2.0%; Score 12; DB 14; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 6.5e+04;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 236 CCTGGTTACCT 247  
 ||:|||||  
 Db 1 CCTGGUACCU 12

RESULT 107  
 US-10-423-311-19/c  
 ; Sequence 19, Application US/10423311  
 ; Publication No. US20030206938A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pereira, Heloise Anne

; APPLICANT: Chodosh, James  
 ; APPLICANT: Callagan, Michelle C.  
 ; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP:  
 ; TITLE OF INVENTION: CAP37 PEPTIDES  
 ; FILE REFERENCE: 6267.002  
 ; CURRENT APPLICATION NUMBER: US/10/423,311  
 ; CURRENT FILING DATE: 2003-04-25  
 ; PRIOR APPLICATION NUMBER: 60/378,295  
 ; PRIOR FILING DATE: 2002-05-03  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely synthesized  
 US-10-423-311-19

Query Match 2.0%; Score 12; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328  
 ||:|||||  
 Db 19 TGAGGATCTTCA 8

RESULT 108  
 US-10-349-143-11302/c  
 ; Sequence 11302, Application US/10349143  
 ; Publication No. US20040005584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Daniel  
 ; APPLICANT: Blumenfeld, Marta  
 ; APPLICANT: Chumakov, Ilya  
 ; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
 ; FILE REFERENCE: GENSET.020CP1  
 ; CURRENT APPLICATION NUMBER: US/10/349,143  
 ; CURRENT FILING DATE: 2003-01-21  
 ; PRIOR APPLICATION NUMBER: US/09/422,978  
 ; PRIOR FILING DATE: 1999-10-20  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
 ; NUMBER OF SEQ ID NOS: 11796  
 ; SEQ ID NO 11302  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: primer\_bind  
 ; LOCATION: 1..19\_bind  
 ; OTHER INFORMATION: downstream amplification primer 99-4077 for SEQ 3437, in complem  
 US-10-349-143-11302

Query Match 2.0%; Score 12; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTCC 187  
 ||:|||||  
 Db 15 TGCTCTTCCTCC 4

RESULT 109  
 US-10-352-179-5/c  
 ; Sequence 5, Application US/10352179  
 ; Publication No. US20040006788A1  
 ; GENERAL INFORMATION:

```
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Oryza minuta
; US-10-352-179-5

Query Match      2.0%; Score 12; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TCTCCGCTACA 193
DB 17 TCTCCGCTACA 6

RESULT 110
US-09-802-669-21/c
; Sequence 21, Application US/09802669
; Patent No. US2002004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-802-669-21

Query Match      2.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGCTCTT 182
DB 20 GGAATTGCTCTT 9

RESULT 111
US-09-887-145-18
; Sequence 18, Application US/09887145
; Publication No. US20030082139A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Seung U
; TITLE OF INVENTION: Immortalized human microglia
; cell and continuous cell line
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387

; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Microsoft Word version 97
; CURRENT APPLICATION NUMBER: US/09/887,145
; FILING DATE: 22-Jun-2001
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: UBC-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-887-145-18

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGGA 445
DB 9 TTACTGCTGGA 20

RESULT 112
US-09-910-185-34
; Sequence 34, Application US/09910185
; Publication No. US20030083279A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3 EXPRESSION
; FILE REFERENCE: RFS-0258
; CURRENT APPLICATION NUMBER: US/09/910,185
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-910-185-34

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGAC 354
DB 9 TTCTGTGAGGAC 20

RESULT 113
US-09-851-871-14
; Sequence 14, Application US/09851871
; Publication No. US20030176374A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
```

```
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0543
; CURRENT APPLICATION NUMBER: US/09/851,871
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-14

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGGAGCCCC 258
Db      6 TCCTGGAGCCCC 17

RESULT 114
US-09-851-871-198
; Sequence 198, Application US/09851871
; Publication No. US20030176374A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0543
; CURRENT APPLICATION NUMBER: US/09/851,871
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-198

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGGAGCCCC 258
Db      5 TCCTGGAGCCCC 16

RESULT 115
US-10-619-220-21/c
; Sequence 21, Application US/10619220
```

```
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-619-220-21

Query Match      2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      171 GGAATTCCTCTT 182
Db      20 GGAATTCCTCTT 9

RESULT 116
US-10-068-160-43/c
; Sequence 43, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-43

Query Match      2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      255 CCCCTGCTACGA 266
Db      18 CCCCTGCTACGA 7

RESULT 117
US-10-271-887-172
; Sequence 172, Application US/10271887
```

Publication No. US20030087871A1  
 GENERAL INFORMATION:  
 APPLICANT: Hong Zhang  
 APPLICANT: Andrew T. Watt  
 TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION  
 FILE REFERENCE: RTS-0183  
 CURRENT APPLICATION NUMBER: US/10/271,887  
 CURRENT FILING DATE: 2002-10-15  
 PRIOR APPLICATION NUMBER: US/09/659,845A  
 PRIOR FILING DATE: 2001-07-23  
 NUMBER OF SEQ ID NOS: 174  
 SEQ ID NO 172  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-271-887-172

Query Match 2.0%; Score 12; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGAGGAGGATT 32  
 |||||  
 Db 5 CCGAGGAGGATT 16

RESULT 118  
 US-10-003-354-41/c  
 Sequence 41, Application US/10003354  
 Publication No. US20030114400A1  
 GENERAL INFORMATION:  
 APPLICANT: C. Frank Bennett  
 APPLICANT: Susan M. Freier  
 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE  
 FILE REFERENCE: RTS-0348  
 CURRENT APPLICATION NUMBER: US/10/003,354  
 CURRENT FILING DATE: 2001-12-06  
 NUMBER OF SEQ ID NOS: 89  
 SEQ ID NO 41  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-003-354-41

Query Match 2.0%; Score 12; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACAGCCTCTTGA 16  
 |||||  
 Db 12 ACAGCCTCTTGA 1

RESULT 119  
 US-10-006-883A-76/c  
 Sequence 76, Application US/10006883A  
 Publication No. US20030119767A1  
 GENERAL INFORMATION:  
 APPLICANT: Kenneth W. Dobie  
 TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION  
 FILE REFERENCE: RTS-0337  
 CURRENT APPLICATION NUMBER: US/10/006,883A  
 CURRENT FILING DATE: 2001-12-05  
 NUMBER OF SEQ ID NOS: 96  
 SEQ ID NO 76  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-883A-76

Query Match 2.0%; Score 12; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TTTGGGACTTTG 596  
 |||||  
 Db 16 TTTGGGACTTTG 5

RESULT 120  
 US-10-008-789-89  
 Sequence 89, Application US/10008789  
 Publication No. US20030125276A1  
 GENERAL INFORMATION:  
 APPLICANT: C. Frank Bennett  
 APPLICANT: Kenneth Dobie  
 TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EX  
 FILE REFERENCE: RTS-0333  
 CURRENT APPLICATION NUMBER: US/10/008,789  
 CURRENT FILING DATE: 2001-11-08  
 NUMBER OF SEQ ID NOS: 89  
 SEQ ID NO 89  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-008-789-89

Query Match 2.0%; Score 12; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGCT 262  
 |||||  
 Db 4 GGAGCCCTGCT 15

RESULT 121  
 US-10-321-555-6  
 Sequence 6, Application US/10321555  
 Publication No. US20030134315A1  
 GENERAL INFORMATION:  
 APPLICANT: Warenius, Hilmar Meek  
 APPLICANT: Seabra, Laurence Anthony  
 TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED U  
 TITLE OF INVENTION: EXPRESSION OF NEGATIVE AND POSITIVE SIGNAL TRANSDUCTION FACTORS  
 FILE REFERENCE: 1417-188  
 CURRENT APPLICATION NUMBER: US/10/321,555  
 CURRENT FILING DATE: 2002-12-18  
 PRIOR APPLICATION NUMBER: US/09/622,277  
 PRIOR FILING DATE: 2000-10-25  
 PRIOR APPLICATION NUMBER: PCT/GB99/00500  
 PRIOR FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: GB 9903035.5  
 PRIOR FILING DATE: 1999-02-10  
 PRIOR APPLICATION NUMBER: GB 9814545.1  
 PRIOR FILING DATE: 1998-07-03  
 PRIOR APPLICATION NUMBER: GB 9812151.0  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: GB 9803447.3  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: GB 9803446.5  
 PRIOR FILING DATE: 1998-02-18  
 NUMBER OF SEQ ID NOS: 15  
 SEQ ID NO 6  
 SOFTWARE: PatentIn version 3.1  
 LENGTH: 20  
 TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR and DNA sequencing primer for exon 5 antisense
US-10-321-555-6

Query Match          2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
    |||||
Db 9 TCGTCTCTCCAG 20

RESULT 122
US-10-084-839-3772
; Sequence 3772, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamachev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPO
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3772
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3772

Query Match          2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 TTTTACTGCTGG 444
    |||||
Db 4 TTTTACTGCTGG 15

RESULT 123
US-10-448-836-61
; Sequence 61, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min

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; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: oligonucleotide for detection and identification of Mycobacteri
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,836
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium vaccae
US-10-448-836-61

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGGCGGTG 76
    |||||
Db 5 AGGTCGGCGGTG 16

RESULT 124
US-10-175-627-16/c
; Sequence 16, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; APPLICANT: Edward A. Dennis
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINAS
; FILE REFERENCE: PTS-0005
; CURRENT APPLICATION NUMBER: US/10/175,627
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-175-627-16

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGGCTGCACC 391
    |||||
Db 12 GCGGCTGCACC 1

RESULT 125
US-10-348-073A-17/c
; Sequence 17, Application US/10348073A
; Publication No. US20030232777A1
; GENERAL INFORMATION:

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; APPLICANT: Marcusson, Eric G.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type 11 Beta
; TITLE OF INVENTION: Inhibitors For Inhibiting Angiogenesis
; FILE REFERENCE: ISPH-0757
; CURRENT APPLICATION NUMBER: US/10/348,073A
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 10/175,627
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-073A-17

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGCGGTGCACC 391
      |||||
Db 12 GCGCGGTGCACC 1

RESULT 126
US-10-448-914A-61
; Sequence 61, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,914A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium vaccae
US-10-448-914A-61

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGCGCGTG 76
      |||||
Db 5 AGGTCGCGCGTG 16

RESULT 127
```

```
US-10-178-258-37/c
; Sequence 37, Application US/10178258
; Publication No. US20030235913A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEME OXYGENASE 1 EXPRESSION
; FILE REFERENCE: HTS-0010
; CURRENT APPLICATION NUMBER: US/10/178,258
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-178-258-37

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 ACCGCAAGGCTG 364
      |||||
Db 12 ACCGCAAGGCTG 1

RESULT 128
US-10-178-258-61
; Sequence 61, Application US/10178258
; Publication No. US20030235913A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEME OXYGENASE 1 EXPRESSION
; FILE REFERENCE: HTS-0010
; CURRENT APPLICATION NUMBER: US/10/178,258
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-178-258-61

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 ACCGCAAGGCTG 364
      |||||
Db 9 ACCGCAAGGCTG 20

RESULT 129
US-10-283-443-19/c
; Sequence 19, Application US/10283443
; Publication No. US20040005580A1
; GENERAL INFORMATION:
; APPLICANT: Neo Gen Screening, Inc.
; TITLE OF INVENTION: Detecting Mutations in the GALT Gene by DNA Melting Curve Analysis
; FILE REFERENCE: 2144
; CURRENT APPLICATION NUMBER: US/10/283,443
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-443-19

Query Match          2.0%; Score 12; DB 15; Length 20;
```



```
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 GAGCCCTCTGCTA 263
Db 17 GAGCCCTCTGCTA 6

RESULT 130
US-10-349-143-11732/c
; Sequence 11732, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11732
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20_
; OTHER INFORMATION: downstream amplification primer 99-4029 for SEQ 3867, in compleme
US-10-349-143-11732

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 CGTCTCTCCAGA 522
Db 14 CGTCTCTCCAGA 3

RESULT 131
US-10-289-762-1338
; Sequence 1338, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; FILE REFERENCE: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1338
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1338

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CTGAGGATCTTC 327
Db 316 CTGAGGATCTTC 327

RESULT 132
US-10-352-179-69/c
; Sequence 69, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-69

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TCCTCCGCTACA 193
Db 18 TCCTCCGCTACA 7

RESULT 133
US-10-210-290-65/c
; Sequence 65, Application US/10210290
; Publication No. US20040023378A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Eric G. Marcussen
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,290
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-65

Query Match 2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 GCGCGGCTGCA 389
Db 16 GCGCGGCTGCA 5

RESULT 134
US-10-210-479-17/c
; Sequence 17, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
```

```
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-17

Query Match          2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GCTGCGGGCGCT 386
Db      18 GCTGCGGGCGCT 7

RESULT 135
US-10-210-479-91
; Sequence 91, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-210-479-91

Query Match          2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GCTGCGGGCGCT 386
Db      3 GCTGCGGGCGCT 14

RESULT 136
US-10-444-206-14
; Sequence 14, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-444-206-14

Query Match          2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      375 GCTGCGGGCGCT 386
Db      3 GCTGCGGGCGCT 14
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-14

Query Match          2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGGAGCCCC 258
Db      6 TCCTGGAGCCCC 17

RESULT 137
US-10-444-206-198
; Sequence 198, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-198

Query Match          2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGGAGCCCC 258
Db      5 TCCTGGAGCCCC 16

RESULT 138
US-10-100-957A-69/c
; Sequence 69, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-6
US-10-100-957A-69/c
```

; OTHER INFORMATION: substrate recognition sequence  
US-10-100-957A-69

Query Match 1.8%; Score 11; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCTGT 348  
|||||  
DB 11 TCTACTTCTGT 1

RESULT 139

US-10-091-281-187/c  
; Sequence 187, Application US/10091281  
; Publication No. US20030190617A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYMOND, VINCENT  
; APPLICANT: SI, ERWIN  
; APPLICANT: MORISSETTE, JEAN  
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: 13587.338  
; CURRENT APPLICATION NUMBER: US/10/091,281  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 187  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Putative ETSP/GABP.01 motif  
US-10-091-281-187

Query Match 1.8%; Score 11; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 GCTCTTCTCTCC 187  
|||||  
DB 11 GCTCTTCTCTCC 1

RESULT 140

US-08-591-486B-97  
; Sequence 97, Application US/08591486B  
; Publication No. US20020037866A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlöngensiepen, Georg F  
; APPLICANT: Schlöngensiepen, Reimar  
; APPLICANT: Schlöngensiepen, Karl-Hermann  
; APPLICANT: Göttingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition  
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment  
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the  
; TITLE OF INVENTION: Treatment of Neoplasms  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,486B  
; FILING DATE: 11-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93111059.7  
; FILING DATE: 10-JUL-1993  
; PRIOR APPLICATION DATA: PCT/EP94/02218  
; APPLICATION NUMBER: PCT/EP94/02218  
; FILING DATE: 6-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10496/P60122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-9350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-591-486B-97

Query Match 1.8%; Score 11; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 TCATGACCTTC 423  
|||||  
DB 2 TCATGACCTTC 12

RESULT 141

US-09-504-231A-1366  
; Sequence 1366, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: TPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1366  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-1366

Query Match 1.8%; Score 11; DB 9; Length 14;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 216 TGCCCGCTGCT 226  
:|||||:  
DB 1 UGCCCGCUGCU 11

## RESULT 142

US-09-274-553D-1366  
; Sequence 1366, Application US/09274553D  
; Patent No. US2002008225A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1366  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-1366

Query Match 1.8%; Score 11; DB 9; Length 14;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 216 TGGCCGCTGCT 226

Db 1 UGGCGCGUGU 11

## RESULT 143

US-10-108-714-1  
; Sequence 1, Application US/10108714  
; Publication No. US20020128445A1  
; GENERAL INFORMATION:  
; APPLICANT: Regan, John W.  
; APPLICANT: Gil, Daniel W.  
; APPLICANT: Woodward, David F.  
; TITLE OF INVENTION: No. US20020128445A1 Human Prostaglandin EP Receptor  
; FILE REFERENCE: 17023 DIV CIP  
; CURRENT APPLICATION NUMBER: US/10/108,714  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431  
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-714-1

Query Match 1.8%; Score 11; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCC 256

Db 3 CTCCTGGAGCC 13

## RESULT 144

US-09-504-231A-55/c  
; Sequence 55, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 55  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-55

Query Match 1.8%; Score 11; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 AGGCTGAGCCC 369

Db 13 AGGCTGAGCCC 3

## RESULT 145

US-09-504-231A-610  
; Sequence 610, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 610  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-610

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      57 CTGGGCTAAGG 67
Db      1 CUGGGCUAAGG 11

RESULT 146
US-09-274-553D-55/c
; Sequence 55, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: FPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-55

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      359 AGGCTGAGCCC 369
Db      13 AGGCTGAGCCC 3

RESULT 147
US-09-274-553D-610
; Sequence 610, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: FPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
```

```
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 610
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-610

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      57 CTGGGCTAAGG 67
Db      1 CUGGGCUAAGG 11

RESULT 148
US-09-918-728B-13/c
; Sequence 13, Application US/09918728B
; Publication No. US20030105308A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleoside Triphosphates and Their Incorporation into Oligonucle
; FILE REFERENCE: MHB00-831-H (400/033)
; CURRENT APPLICATION NUMBER: US/09/918,728B
; CURRENT FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-918-728B-13

Query Match      1.8%; Score 11; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      324 CTTACCGCGC 334
Db      11 CTTACCGCGC 1

RESULT 149
US-09-918-728B-14/c
; Sequence 14, Application US/09918728B
; Publication No. US20030105308A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleoside Triphosphates and Their Incorporation into Oligonucle
; FILE REFERENCE: MHB00-831-H (400/033)
; CURRENT APPLICATION NUMBER: US/09/918,728B
; CURRENT FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-918-728B-14

Query Match      1.8%; Score 11; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      385 CTGACCGCGC 395
```

Db 11 CTGACCGCGC 1  
|||||

## RESULT 150

US-09-793-146-32/c  
; Sequence 32, Application US/09793146  
; Publication No. US20030203359A1

## GENERAL INFORMATION:

; APPLICANT: UHLMANN, EUGEN  
; APPLICANT: BREIPOHL, GERHARD  
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 02481.1437-02  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: P 44 08 528.1  
; PRIOR FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: 08/402,838  
; PRIOR FILING DATE: 1995-03-13  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA  
US-09-793-146-32

## Query Match

Best Local Similarity 1.8%; Score 11; DB 11; Length 15;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 CCTGGAGCCCC 258  
|||||

Db 11 CCTGGAGCCCC 1

## RESULT 151

US-10-287-919-1850  
; Sequence 1850, Application US/10287919  
; Publication No. US20030085830A1

## GENERAL INFORMATION:

; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 1850  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (1074273)...(1074288)  
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 2348  
US-10-287-919-1850

## Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 GAGGTTGATGA 563  
|||||

Db 4 GAGGTTGATGA 14

## RESULT 152

US-10-156-306-7865  
; Sequence 7865, Application US/10156306  
; Publication No. US20030119017A1

## GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McGSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MEHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 7865  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-7865

## Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 177 GCTCTTCCTCC 187  
|||:|:|

Db 5 GCUCUCCUCC 15

## RESULT 153

US-10-292-198-64/c  
; Sequence 64, Application US/10292198  
; Publication No. US20030157654A1

## GENERAL INFORMATION:

; APPLICANT: SHEN, Ben  
; APPLICANT: LIU, Wen  
; TITLE OF INVENTION: BIOSYTHESIS OF ENEDIYNE COMPOUNDS BY MANIPULATION OF C-1027 GENE  
; TITLE OF INVENTION: PATHWAY  
; FILE REFERENCE: 054030-0007  
; CURRENT APPLICATION NUMBER: US/10/292,198  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: US 10/159,257  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 09/478,188  
; PRIOR FILING DATE: 2000-01-05  
; PRIOR APPLICATION NUMBER: US 60/115,434  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 64  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Streptomyces globisporus  
US-10-292-198-64

## Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 TTCACCTCCTG 251  
|||||

Db 12 TTCACCTCCTG 2

## RESULT 154

US-10-084-839-3873  
; Sequence 3873, Application US/10084839  
; Publication No. US20030186238A1

## GENERAL INFORMATION:

; APPLICANT: Third Wave Technologies  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Argue, Brad T.  
; APPLICANT: Bartholomay, Christian T.  
; APPLICANT: Chenak, JoAnne  
; APPLICANT: Curtis, Michelle L.  
; APPLICANT: Eis, Peggy S.  
; APPLICANT: Hall, Jeff G.

; APPLICANT: Ip, Hon S.  
; APPLICANT: Ji, Lin  
; APPLICANT: Kaiser, Michael  
; APPLICANT: Kwiatkowski, Jr., Robert W.  
; APPLICANT: Lukowiak, Andrew A.  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Lyamacheva, Natalie E.  
; APPLICANT: Ma, WuPo  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Olson, Sarah M.  
; APPLICANT: Olson-Munoz, Marilyn C.  
; APPLICANT: Schaefer, James J.  
; APPLICANT: Skrzypczynski, Zbigniew  
; APPLICANT: Takova, Tsetska Y.  
; APPLICANT: Thompson, Lisa C.  
; APPLICANT: Vedvik, Kevin L.  
; TITLE OF INVENTION: RNA Detection Assays  
; FILE REFERENCE: FORS-06666  
; CURRENT APPLICATION NUMBER: US/10/084,839  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 4004  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3873  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-084-839-3873

Query Match 1.8%; Score 11; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 TGAGCCCGAGG 373  
|||||  
Db 1 TGAGCCCGAGG 11

RESULT 155  
US-10-091-281-3/c  
; Sequence 3, Application US/10091281  
; Publication No. US20030190617A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYMOND, VINCENT  
; APPLICANT: SI, ERWIN  
; APPLICANT: MORISSETTE, JEAN  
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: 13587.338  
; CURRENT APPLICATION NUMBER: US/10/091,281  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Putative OCTB/TST1.01 motif  
US-10-091-281-3

Query Match 1.8%; Score 11; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GTGGAATTGCT 179  
|||||  
Db 12 GTGGAATTGCT 2

RESULT 156  
US-10-440-850-313  
; Sequence 313, Application US/10440850

; Publication No. US20030207837A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rev  
; FILE REFERENCE: 250/130 (MEHB00-900-A)  
; CURRENT APPLICATION NUMBER: US/10/440,850  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/650,012  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 08/585,684  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: US 60/000,951  
; PRIOR FILING DATE: 1995-07-07  
; PRIOR APPLICATION NUMBER: US 09/038,073  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 2285  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 313  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-440-850-313

Query Match 1.8%; Score 11; DB 15; Length 15;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428  
|||||  
Db 4 ACCUCAAAGA 14

RESULT 157  
US-10-440-850-314  
; Sequence 314, Application US/10440850  
; Publication No. US20030207837A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rev  
; FILE REFERENCE: 250/130 (MEHB00-900-A)  
; CURRENT APPLICATION NUMBER: US/10/440,850  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/650,012  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 08/585,684  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: US 60/000,951  
; PRIOR FILING DATE: 1995-07-07  
; PRIOR APPLICATION NUMBER: US 09/038,073  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 2285  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 314  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-440-850-314

Query Match 1.8%; Score 11; DB 15; Length 15;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428  
|||||  
Db 3 ACCUCAAAGA 13

## RESULT 158

US-10-440-850-767  
; Sequence 767, Application US/10440850  
; Publication No. US20030207837A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Reversal  
; TITLE OF INVENTION: Immune Responses  
; FILE REFERENCE: 250/130 (MEHB00-900-A)  
; CURRENT APPLICATION NUMBER: US/10/440,850  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/650,012  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 08/585,684  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: US 60/000,951  
; PRIOR FILING DATE: 1995-07-07  
; PRIOR APPLICATION NUMBER: US 09/038,073  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 2285  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 767  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-440-850-767

Query Match 1.8%; Score 11; DB 15; Length 15;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATTCAAAAT 51

Db 5 AAUUCAAAAU 15

## RESULT 159

US-10-453-792-20/c  
; Sequence 20, Application US/10453792  
; Publication No. US20040029110A1  
; GENERAL INFORMATION:  
; APPLICANT: STUYVER, LIEVEN  
; APPLICANT: ROSSAU, RUDI  
; APPLICANT: MAERTENS, GEERT  
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV  
; NUMBER OF SEQUENCES: 313  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/453,792  
; FILING DATE: 04-Jun-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/155,885A  
; FILING DATE: 08-Oct-1998  
; APPLICATION NUMBER: PCT/EP97/02002  
; FILING DATE: 21-APR-1997  
; APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 2551-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-453-792-20

Query Match 1.8%; Score 11; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 ACTGCTGGAAT 447

Db 13 ACTGCTGGAAT 3

## RESULT 160

US-09-866-108-932  
; Sequence 932, Application US/09866108  
; Patent No. US2002004800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEONICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,697  
; PRIOR FILING DATE: 2000-09-21





; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 60/266,860  
 ; PRIOR FILING DATE: 2001-02-05  
 ; NUMBER OF SEQ ID NOS: 15752  
 ; SOFTWARE: Aemica Sequence Listing Engine  
 ; SEQ ID NO 936  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-866-108-936

Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy 359 AGCGTGAGCCC 369  
 Db 3 AGCGTGAGCCC 13  
 |||||  
 |||||

RESULT 165  
 US-09-866-108-937  
 ; Sequence 937, Application US/09866108  
 ; Patent No. US2002004800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang  
 ; APPLICANT: PENN, Sharon G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359

;  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 937  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-937

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGCGTGAGCCC 369  
|||||  
DB 2 AGCGTGAGCCC 12

RESULT 166  
US-09-866-108-938  
; Sequence 938, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665

;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 938  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-938

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGCGTGAGCCC 369  
|||||  
DB 1 AGCGTGAGCCC 11

RESULT 167  
US-09-866-108-1462  
; Sequence 1462, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1462
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1462

```

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels

QY 482 CCTGGGAAGG 492  
|||  
Db 7 CCTGGGAAGG 17

RESULT 168  
US-09-866-108-1463  
; Sequence 1463, Application US/09866108  
; Patent No. US2002048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

```

; ORGANISM: Homo sapiens
US-09-866-108-1463

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels

Qy      482 CCTGGGAAGGG 492
      |||||
Db      6 CCTGGGAAGGG 16

```

RESULT 169  
US-09-866-108-1464  
Sequence 1464, Application US/09866108  
Patent No. US20030048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: A60MICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27

```

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred.NC.2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      482  CCTGGGAAGGG 492
          |||||
Db       5    CCTGGGAAGGG 15

```

## RESULT 170

US-09-866-108-1465  
; Sequence 1465, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David R.  
; APPLICANT: RANK, David K.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US 60/207,456  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1465  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-1465

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy 482 CCTGGGAAGG 492

Db 4 CCTGGGAAGG 14  
|||||

## RESULT 171

US-09-866-108-1466  
; Sequence 1466, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1466  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-1466

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy 482 CCTGGGAAGG 492

Db 3 CCTGGGAAGG 13  
|||||

## RESULT 172

US-09-866-108-1467  
; Sequence 1467, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1467  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-1467

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492  
|||||  
Db 2 CCTGGGAAGGG 12

RESULT 173  
US-09-866-108-1468  
; Sequence 1468, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1468  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-1468

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492  
|||||  
Db 1 CCTGGGAAGGG 11

RESULT 174  
US-09-866-108-7363  
; Sequence 7363, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 7363  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7363

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGT 509  
|||||  
Db 7 GAAATTCAGT 17

## RESULT 175

US-09-866-108-7370  
; Sequence 7370, Application US/09866108  
; Patent No. US20020048800A1

## GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 7370  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7370

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTCAGTT 510  
|||||  
Db 1 AAAATTCAGTT 11

## RESULT 176

US-09-866-108-9635/c  
; Sequence 9635, Application US/09866108  
; Patent No. US20020048800A1

## GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 9635  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9635

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188  
 Db 17 CTCCTCTCCG 7

RESULT 177

US-09-866-108-9636/c  
 ; Sequence 9636, Application US/09866108  
 ; Patent No. US2002004800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang  
 ; APPLICANT: PENN, Sharon G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEOMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 60/266,860  
 ; PRIOR FILING DATE: 2001-02-05  
 ; NUMBER OF SEQ ID NOS: 15752  
 ; SOFTWARE: Aecomica Sequence Listing Engine  
 ; SEQ ID NO 9636  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-866-108-9636

Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188  
 Db 16 CTCCTCTCCG 6

RESULT 178

US-09-866-108-9637/c  
 ; Sequence 9637, Application US/09866108  
 ; Patent No. US2002004800A1  
 ; GENERAL INFORMATION:

APPLICANT: GU, Yizhong  
 APPLICANT: JI, Yonggang  
 APPLICANT: PENN, Sharon G.  
 APPLICANT: HANZEL, David K.  
 APPLICANT: RANK, David R.  
 APPLICANT: CHEN, Wensheng  
 APPLICANT: SHANNON, Mark  
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 FILE REFERENCE: AEOMICA-7  
 CURRENT APPLICATION NUMBER: US/09/866,108  
 CURRENT FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 60/266,860  
 PRIOR FILING DATE: 2001-02-05  
 NUMBER OF SEQ ID NOS: 15752  
 SOFTWARE: Aecomica Sequence Listing Engine  
 SEQ ID NO 9637  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-866-108-9637

Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188  
 Db 15 CTCCTCTCCG 5

RESULT 179  
 US-09-866-108-9638/c  
 ; Sequence 9638, Application US/09866108  
 ; Patent No. US2002004800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang  
 ; APPLICANT: PENN, Sharon G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEOMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108



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/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecmica Sequence Listing Engine
/ SEQ ID NO 9638
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108-9638
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Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 178 CTCTTCCTCCG 188
Db 14 CTCTTCCTCCG 4
```

```
RESULT 180
US-09-866-108-9639/c
/ Sequence 9639, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecmica Sequence Listing Engine
/ SEQ ID NO 9639
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108-9639
```

```
Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 178 CTCTTCCTCCG 188
Db 13 CTCTTCCTCCG 3
```

```
RESULT 181
US-09-866-108-9640/c
/ Sequence 9640, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
```

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Query Match	1.8%	Score 11;	DB 9;	Length 17;	Best Local Similarity	100.0%;	Pred. No. 2.3e+05;	
Matches 11;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
<p>US-09-866-108-9641</p> <p>Query Match</p> <p>Best Local Similarity</p> <p>Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								
QY	178	CTCTTCCTCCG	188					
DB	11	CTCTTCCTCCG	1					
<p>RESULT 183</p> <p>US-09-827-998-183</p> <p>Sequence 183, Application US/09827998</p> <p>Patent No. US20020102252A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Gu, Yizhong</p> <p>APPLICANT: Shannon, Mark</p> <p>TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E</p> <p>FILE REFERENCE: MDMORF-8</p> <p>CURRENT APPLICATION NUMBER: US/09/827,998</p> <p>CURRENT FILING DATE: 2001-04-06</p> <p>PRIOR APPLICATION NUMBER: US 60/207,456</p> <p>PRIOR FILING DATE: 2000-05-26</p> <p>PRIOR APPLICATION NUMBER: US 60/236,359</p> <p>PRIOR FILING DATE: 2000-09-27</p> <p>NUMBER OF SEQ ID NOS: 1881</p> <p>SOFTWARE: Acomica Sequence Listing Engine</p> <p>SEQ ID NO 183</p> <p>LENGTH: 17</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-827-998-183</p>								
QY	426	AGATTATTTT	436					
DB	7	AGATTATTTT	17					
<p>Query Match</p> <p>Best Local Similarity</p> <p>Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>								
<p>US-09-827-998-184</p> <p>Sequence 184, Application US/09827998</p> <p>Patent No. US20020102252A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Gu, Yizhong</p> <p>APPLICANT: Shannon, Mark</p> <p>TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E</p> <p>FILE REFERENCE: MDMORF-8</p> <p>CURRENT APPLICATION NUMBER: US/09/827,998</p> <p>CURRENT FILING DATE: 2001-04-06</p> <p>PRIOR APPLICATION NUMBER: US 60/207,456</p> <p>PRIOR FILING DATE: 2000-05-26</p> <p>PRIOR APPLICATION NUMBER: US 60/236,359</p> <p>PRIOR FILING DATE: 2000-09-27</p> <p>NUMBER OF SEQ ID NOS: 1881</p> <p>SOFTWARE: Acomica Sequence Listing Engine</p> <p>SEQ ID NO 184</p> <p>LENGTH: 17</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-827-998-184</p>								

```
Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 6 AGATTATTTT 16

RESULT 185
US-09-827-998-185
; Sequence 185, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-185

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 5 AGATTATTTT 15

RESULT 186
US-09-827-998-186
; Sequence 186, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 186
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-186

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 4 AGATTATTTT 14

RESULT 187
US-09-827-998-187
; Sequence 187, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 187
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-187

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 3 AGATTATTTT 13

RESULT 188
US-09-827-998-188
; Sequence 188, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 188
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-188

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 2 AGATTATTTT 12

RESULT 189
US-09-827-998-189
; Sequence 189, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
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; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 189  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-189

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 AGATTATTTT 436  
|||||  
Db 1 AGATTATTTT 11

RESULT 190  
US-09-827-998-345  
; Sequence 345, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDHMOF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 345  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-345

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 425 AGATTATTTT 435  
|||||  
Db 7 AGATTATTTT 17

RESULT 191  
US-09-827-998-346  
; Sequence 346, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDHMOF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 346

; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-346

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 425 AGATTATTTT 435  
|||||  
Db 6 AGATTATTTT 16

RESULT 192  
US-09-827-998-347  
; Sequence 347, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDHMOF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 347  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-347

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 425 AGATTATTTT 435  
|||||  
Db 5 AGATTATTTT 15

RESULT 193  
US-09-827-998-348  
; Sequence 348, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDHMOF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 348  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-348

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 425 AAGATTATTTT 435
Db 4 AAGATTATTTT 14

RESULT 194
US-09-827-998-349
; Sequence 349, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 349
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-349

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 3 AAGATTATTTT 13

RESULT 195
US-09-827-998-350
; Sequence 350, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 350
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-350

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 2 AAGATTATTTT 12

RESULT 196
US-09-827-998-351
; Sequence 351, Application US/09827998
; Patent No. US20020102252A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 351
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-351

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 1 AAGATTATTTT 11

RESULT 197
US-09-827-998-648/c
; Sequence 648, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 648
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-648

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 CTACCTGTGCT 91
Db 17 CTACCTGTGCT 7

RESULT 198
US-09-827-998-649/c
; Sequence 649, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 649
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-649

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      16 CTACCTGTGCT 6

RESULT 199
US-09-827-998-650/c
; Sequence 650, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 650
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-650

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      15 CTACCTGTGCT 5

RESULT 200
US-09-827-998-651/c
; Sequence 651, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 651
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-651

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      12 CTACCTGTGCT 2

RESULT 201
US-09-827-998-652/c
; Sequence 652, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 652
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-652

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      13 CTACCTGTGCT 3

RESULT 202
US-09-827-998-653/c
; Sequence 653, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 653
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-653

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      12 CTACCTGTGCT 2
```

RESULT 203  
US-09-827-998-654/c  
; Sequence 654, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 654  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-654

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 CTACCTGTGCT 91  
|||||  
Db 11 CTACCTGTGCT 1

RESULT 204  
US-09-872-462-46  
; Sequence 46, Application US/09872462  
; Patent No. US20020169295A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Corrigan, Amy  
; TITLE OF INVENTION: HUMAN NEDD1  
; FILE REFERENCE: AECOMICA-9  
; CURRENT APPLICATION NUMBER: US/09/872,462  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 473  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 46  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-872-462-46

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GAATTGCTCTT 182  
|||||  
Db 7 GAATTGCTCTT 17

RESULT 205  
US-09-872-462-47  
; Sequence 47, Application US/09872462  
; Patent No. US20020169295A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Corrigan, Amy  
; TITLE OF INVENTION: HUMAN NEDD1  
; FILE REFERENCE: AECOMICA-9  
; CURRENT APPLICATION NUMBER: US/09/872,462  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 473  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 47  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-872-462-47

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GAATTGCTCTT 182  
|||||  
Db 6 GAATTGCTCTT 16

RESULT 206  
US-09-872-462-48  
; Sequence 48, Application US/09872462  
; Patent No. US20020169295A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Corrigan, Amy  
; TITLE OF INVENTION: HUMAN NEDD1  
; FILE REFERENCE: AECOMICA-9  
; CURRENT APPLICATION NUMBER: US/09/872,462  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27





; CURRENT APPLICATION NUMBER: US/09/872,462  
 ; CURRENT FILING DATE: 2001-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; NUMBER OF SEQ ID NOS: 473  
 ; SOFTWARE: Acomica Sequence Listing Engine  
 ; SEQ ID NO 51  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-872-462-51

Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GAATTGCTCTT 182  
 |||||  
 Db 2 GAATTGCTCTT 12

RESULT 210  
 US-09-872-462-52  
 ; Sequence 52, Application US/09872462  
 ; Patent No. US20020169295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gl. yizhong  
 ; APPLICANT: Corrigan, Amy  
 ; TITLE OF INVENTION: HUMAN NEDD1  
 ; FILE REFERENCE: ACOMICA-9  
 ; CURRENT APPLICATION NUMBER: US/09/872,462  
 ; CURRENT FILING DATE: 2001-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30  
 ; NUMBER OF SEQ ID NOS: 473  
 ; SOFTWARE: Acomica Sequence Listing Engine  
 ; SEQ ID NO 52  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-872-462-52  
 Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 172 GAATTGCTCTT 182  
 |||||  
 Db 1 GAATTGCTCTT 11  
 RESULT 211  
 US-09-864-785-224  
 ; Sequence 224, Application US/09864785  
 ; Patent No. US2002017568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Draper, Ken  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
 ; FILE REFERENCE: 400/022 (MBH00-812-D)  
 ; CURRENT APPLICATION NUMBER: US/09/864,785  
 ; CURRENT FILING DATE: 2001-05-23  
 ; NUMBER OF SEQ ID NOS: 3929  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 224  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
 US-09-864-785-224

Query Match 1.8%; Score 11; DB 9; Length 17;  
 Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 375 GCTGCGCGGC 385  
 |||||  
 Db 7 GCUGCGCGGC 17  
 RESULT 212  
 US-09-864-785-622  
 ; Sequence 622, Application US/09864785  
 ; Patent No. US2002017568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Draper, Ken  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
 ; FILE REFERENCE: 400/022 (MBH00-812-D)  
 ; CURRENT APPLICATION NUMBER: US/09/864,785  
 ; CURRENT FILING DATE: 2001-05-23  
 ; NUMBER OF SEQ ID NOS: 3929  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 622  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-864-785-622

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553  
|||||:|:|:  
DB 7 GCCCCUGAUG 17

RESULT 213

US-09-864-785-623  
; Sequence 623, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 623  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-623

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553  
|||||:|:|:  
DB 6 GCCCCUGAUG 16

RESULT 214

US-09-864-785-624  
; Sequence 624, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 624  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-624

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553

DB 5 GCCCCUGAUG 15  
|||||:|:|:

RESULT 215

US-09-864-785-625  
; Sequence 625, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 625  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-625

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553  
|||||:|:|:  
DB 4 GCCCCUGAUG 14

RESULT 216

US-09-864-785-1528  
; Sequence 1528, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1528  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-1528

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGGC 385  
|||||:|:|:  
DB 6 GCUGCGCGGC 16

RESULT 217

US-09-864-785-1529  
; Sequence 1529, Application US/09864785

Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1529  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-1529

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385  
|||:|||||  
Db 3 GCUGCGCGCGC 13

RESULT 218  
US-09-864-785-1671  
; Sequence 1671, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1671  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-1671

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553  
|||:|||||  
Db 3 GCCCCUGAUG 13

RESULT 219  
US-09-864-785-2135  
; Sequence 2135, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2135  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-2135

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 72.7%; Pred. No. 2.3e+05;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553  
|||:|||||  
Db 1 GCCCCUGAUG 11

RESULT 220  
US-09-864-785-2779  
; Sequence 2779, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2779  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-2779

Query Match 1.8%; Score 11; DB 9; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385  
|||:|||||  
Db 4 GCUGCGCGCGC 14

RESULT 221  
US-09-864-785-2780  
; Sequence 2780, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of NF-Kappa B  
; FILE REFERENCE: 400/022 (MBH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2780

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2780

Query Match
Best Local Similarity 1.8%; Score 11; DB 9; Length 17;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385
Db 1 GCUGCGCGCGC 11

RESULT 222
US-09-825-805-591/c
; Sequence 591, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MEHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 591
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-591

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGA 253
Db 11 CACCTCCTGGA 1

RESULT 223
US-09-825-805-699/c
; Sequence 699, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
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; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MEHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 699
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-699

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGC 261
Db 13 GGAGCCCTGC 3

RESULT 224
US-09-730-289B-165
; Sequence 165, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MEHB00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 165
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-165

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTTAC 438
Db 7 AUAUUUUUAC 17

RESULT 225
US-09-730-289B-171
; Sequence 171, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
```

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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MEH800-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 171
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-171

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 27.3%; Pred. No. 2.3e+05;
Matches 3; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      429 TTATTTTACT 439
Db      1 UUAUUUUUACU 11

RESULT 226
US-09-818-875-931
; Sequence 931, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-931

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      296 GAGGGAACCCC 306
Db      2 GAGGGAACCCC 12

RESULT 227
US-09-818-875-932/c
; Sequence 932, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

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; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-932

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      296 GAGGGAACCCC 306
Db      16 GAGGGAACCCC 6

RESULT 228
US-09-818-875-3798
; Sequence 3798, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3798
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-3798

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      291 TCTCGGAGGGA 301
Db      4 TCTCGGAGGGA 14

RESULT 229
US-09-818-875-3795/c
; Sequence 3799, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.

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; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Stranded Oligonucleotides
; CURRENT APPLICATION NUMBER: Napro-4
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/181,875
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3799
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-3799

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Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 291 TCTGCGGAGGA 301
      |||||
DB 14 TCTGCGGAGGA 4

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RESULT 230
US-09-780-533A-52/c
; Sequence 52, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-52

```

```

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 362 CTGAGCCCGAG 372
      |||||
DB 11 CTGAGCCCGAG 1

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RESULT 231
US-09-780-533A-57
; Sequence 57, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim

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; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 57
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-57

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Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY 175 TTGCTCTTCCT 185
      :|||:|:|:
DB 4 UUGCUCUCCU 14

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RESULT 232
US-09-780-533A-58
; Sequence 58, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 58
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-58

```

```

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY 175 TTGCTCTTCCT 185
      :|||:|:|:
DB 2 UUGCUCUCCU 12

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RESULT 233
US-09-780-533A-59
; Sequence 59, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797

```

```
/ PRIOR FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 6679
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 59
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-09-780-533A-59

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTGCTCTTCT 185
Db      1 UUGUCUUCUU 11

RESULT 234
US-09-780-533A-943/c
; Sequence 943, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 943
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-943

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      251 GGAGCCCTGC 261
Db      17 GGAGCCCTGC 7

RESULT 235
US-09-780-533A-944/c
; Sequence 944, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 944
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-944

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      251 GGAGCCCTGC 261
Db      17 GGAGCCCTGC 7

RESULT 236
US-09-780-533A-946/c
; Sequence 946, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 946
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-946

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      363 TGAGCCCGAGG 373
Db      17 TGAGCCCGAGG 7

RESULT 237
US-09-780-533A-952
; Sequence 952, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 952
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-952

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTGCTCTTCT 185
```

[illegible][illegible][illegible]



; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MEHB00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2418  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-2418

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGC 261  
|||||  
Db 15 GGAGCCCTGC 5

## RESULT 243

US-09-780-533A-2419/c  
; Sequence 2419, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MEHB00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2419  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-2419

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGC 261  
|||||  
Db 14 GGAGCCCTGC 4

## RESULT 244

US-09-848-754A-921/c  
; Sequence 921, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MEHB00-958-I (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 921  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-09-848-754A-921

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGA 253  
|||||  
Db 17 CACCTCCTGGA 7

## RESULT 245

US-09-848-754A-922/c  
; Sequence 922, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MEHB00-958-I (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 922  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-922

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGA 253  
|||||  
Db 16 CACCTCCTGGA 6

## RESULT 246

US-09-848-754A-2178/c  
; Sequence 2178, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MEHB00-958-I (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2178  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-2178

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGA 253  
|||||  
Db 11 CACCTCCTGGA 1

## RESULT 247

US-09-848-754A-3135/c  
; Sequence 3135, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-I (400/018), 754A
; CURRENT APPLICATION NUMBER: US/09/848, 754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3135
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3135

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      243 CACCTCTCTGGA 253
DB      15 CACCTCTCTGGA 5

RESULT 248
US-09-848-754A-3136/c
; Sequence 3136, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848, 754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3136
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3136

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      243 CACCTCTCTGGA 253
DB      14 CACCTCTCTGGA 4

RESULT 249
US-09-848-754A-3137/c
; Sequence 3137, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848, 754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3137

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      243 CACCTCTCTGGA 253
DB      14 CACCTCTCTGGA 4

RESULT 250
US-09-776-474-201/c
; Sequence 201, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CH
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776, 474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179, 983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 201
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-201

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      343 TTCTGTGAGGA 353
DB      15 TTCTGTGAGGA 5

RESULT 251
US-09-776-474-205
; Sequence 205, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CH
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776, 474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179, 983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 205
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-205

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

QY 32 TTCTTTACCAA 42  
:|:|:|:|:|  
Db 7 UUCUUUACCAA 17

## RESULT 252

US-09-776-474-206  
; Sequence 206, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 206  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-206

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 54.5%; Pred. No. 2.3e+05;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCAA 42  
:|:|:|:|:|  
Db 5 UUCUUUACCAA 15

## RESULT 253

US-09-776-474-207  
; Sequence 207, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 207  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-207

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 54.5%; Pred. No. 2.3e+05;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 32 TTCTTTACCAA 42  
:|:|:|:|:|  
Db 4 UUCUUUACCAA 14

## RESULT 254

US-09-776-474-208  
; Sequence 208, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 208  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-208

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 54.5%; Pred. No. 2.3e+05;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCAA 42  
:|:|:|:|:|  
Db 3 UUCUUUACCAA 13

## RESULT 255

US-09-776-474-571/c  
; Sequence 571, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 571  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-571

Query Match 1.8%; Score 11; DB 10; Length 17;

```
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
Db 17 TTCTGTGAGGA 7

RESULT 256
US-09-776-474-572/c
; Sequence 572, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 572
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-572

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
Db 16 TTCTGTGAGGA 6

RESULT 257
US-09-776-474-573/c
; Sequence 573, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 573
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-573
```

```
Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
Db 14 TTCTGTGAGGA 4

RESULT 258
US-09-776-474-574/c
; Sequence 574, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 574
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-574

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
Db 12 TTCTGTGAGGA 2

RESULT 259
US-09-776-474-582
; Sequence 582, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 582
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-582
```

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 54.5%; Pred. No. 2.3e+05;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCA 42  
Db 6 UUCUUUACCA 16

RESULT 260  
US-09-776-474-583  
; Sequence 583, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Pattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEH800-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 583  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-583

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 54.5%; Pred. No. 2.3e+05;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCA 42  
Db 1 UUCUUUACCA 11

RESULT 261  
US-09-776-474-1146/c  
; Sequence 1146, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Pattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)  
; FILE REFERENCE: MEH800-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1146  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-776-474-1146

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353  
Db 11 TTCTGTGAGGA 1

RESULT 262  
US-09-930-423-478  
; Sequence 478, Application US/09930423  
; Publication No. US20030092003A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: MEH800,918-A 400/027  
; CURRENT APPLICATION NUMBER: US/09/930,423  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 4553  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 478  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-09-930-423-478

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382  
Db 4 GGGGCTGCGGC 14

RESULT 263  
US-09-930-423-1012  
; Sequence 1012, Application US/09930423  
; Publication No. US20030092003A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: MEH800,918-A 400/027  
; CURRENT APPLICATION NUMBER: US/09/930,423  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 4553  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1012  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-09-930-423-1012

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382  
Db 3 GGGGCTGCGGC 13

RESULT 264  
US-09-930-423-1199  
; Sequence 1199, Application US/09930423  
; Publication No. US20030092003A1

```

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1199
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1199

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGCGGC 382
      |||||:||||
Db      6 GGGGCTGCGGC 16

RESULT 265
US-09-930-423-1533
; Sequence 1533, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1533
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1533

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGCGGC 382
      |||||:||||
Db      7 GGGGCTGCGGC 17

RESULT 266
US-09-930-423-1534
; Sequence 1534, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1534
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1534

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Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGCGGC 382
      |||||:||||
Db      1 GGGGCTGCGGC 11

RESULT 267
US-09-780-164-723/c
; Sequence 723, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-723

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      507 AGTTCGTCTCT 517
      |||||:||||
Db      13 AGTTCGTCTCT 3

RESULT 268
US-09-780-164-911/c
; Sequence 911, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 911
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-911

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      507 AGTTCGTCTCT 517
      |||||:||||
Db      15 AGTTCGTCTCT 5

RESULT 269

```

US-09-780-164-912/c  
; Sequence 912, Application US/09780164  
; Publication No. US20030092646A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20  
; CURRENT APPLICATION NUMBER: US/09/780,164  
; FILE REFERENCE: 400/010  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/185,516  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 2603  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 912  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-164-912

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGTTCGTCTCT 517

Db 11 AGTTCGTCTCT 1

## RESULT 270

US-09-780-164-1049/c  
; Sequence 1049, Application US/09780164  
; Publication No. US20030092646A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20  
; FILE REFERENCE: 400/010  
; CURRENT APPLICATION NUMBER: US/09/780,164  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/185,516  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 2603  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1049  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-164-1049

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGTTCGTCTCT 517

Db 15 AGTTCGTCTCT 6

## RESULT 271

US-09-827-395A-19  
; Sequence 19, Application US/09827395A  
; Publication No. US20030113891A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Lawrence Blatt  
; APPLICANT: James McSwiggen  
; APPLICANT: Bharat Chowhira  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor  
; FILE REFERENCE: MEH800-878-C (400/017)  
; CURRENT APPLICATION NUMBER: US/09/827,395A

; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/780,533  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2617  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-827-395A-19

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255

Db 6 CCUCCUGGAGC 16

## RESULT 272

US-09-827-395A-195  
; Sequence 195, Application US/09827395A  
; Publication No. US20030113891A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Lawrence Blatt  
; APPLICANT: James McSwiggen  
; APPLICANT: Bharat Chowhira  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor  
; FILE REFERENCE: MEH800-878-C (400/017)  
; CURRENT APPLICATION NUMBER: US/09/827,395A  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/780,533  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2617  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 195  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-827-395A-195

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255

Db 7 CCUCCUGGAGC 17

## RESULT 273

US-09-827-395A-196  
; Sequence 196, Application US/09827395A  
; Publication No. US20030113891A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Lawrence Blatt  
; APPLICANT: James McSwiggen  
; APPLICANT: Bharat Chowhira  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor  
; FILE REFERENCE: MEH800-878-C (400/017)  
; CURRENT APPLICATION NUMBER: US/09/827,395A  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/780,533  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,797  
; PRIOR FILING DATE: 2000-02-11

```

; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-196

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
DB 5 CCUCUGGAGC 15

RESULT 274
US-09-827-395A-197
; Sequence 197, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 197
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-197

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
DB 4 CCUCUGGAGC 14

RESULT 275
US-09-827-395A-879
; Sequence 879, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 879
; LENGTH: 17
; TYPE: RNA

```

```

; ORGANISM: Homo sapiens
; US-09-827-395A-879

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
DB 3 CCUCUGGAGC 13

RESULT 276
US-09-827-395A-880
; Sequence 880, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 880
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-880

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
DB 2 CCUCUGGAGC 12

RESULT 277
US-09-740-332-345
; Sequence 345, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
; US-09-740-332-345

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```



QY 57 CTGGGCTAAGG 67  
Db 5 CUGGGCUAAGG 15

RESULT 278  
US-09-740-332-916  
; Sequence 916, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 916  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-916

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGCGGGCT 386  
Db 7 CUGGGCGGCU 17

RESULT 279  
US-09-740-332-917  
; Sequence 917, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 917  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-917

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGCGGGCT 386  
Db 4 CUGGGCGGCU 14

RESULT 280  
US-09-740-332-918  
; Sequence 918, Application US/09740332  
; Publication No. US20030125270A1

; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 918  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-918

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGCGGGCT 386  
Db 1 CUGGGCGGCU 11

RESULT 281  
US-09-740-332-3638/c  
; Sequence 3638, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3638  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-3638

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGCGGGCT 386  
Db 15 CTGGCGGGCT 5

RESULT 282  
US-09-740-332-3639/c  
; Sequence 3639, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patentin version 3.0

```
; SEQ ID NO 3639
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3639

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGCGGGCT 386
Db 12 CTGCGGGCT 2

RESULT 283
US-09-740-332-4210/c
; Sequence 4210, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4210
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4210

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 CTGGGCTAAGG 67
Db 14 CTGGGCTAAGG 4

RESULT 284
US-09-792-818-122
; Sequence 122, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-09-792-818-122

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 515 TCTCCAGACAG 525
Db 6 UCUCACAGACAG 16

RESULT 285
US-09-792-818-310
; Sequence 310, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 310
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-310

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 515 TCTCCAGACAG 525
Db 7 UCUCACAGACAG 17

RESULT 286
US-09-792-818-311
; Sequence 311, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 311
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-311

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 515 TCTCCAGACAG 525
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Db      5 UCUCGACAG 15
      :|:|||||
RESULT 287
US-09-792-818-312
; Sequence 312, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 312
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-312
      Query Match      1.8%; Score 11; DB 10; Length 17;
      Best Local Similarity 81.8%; Pred. No. 2.3e+05;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 TCTCCGACAG 525
      :|:|||||
Db      4 UCUCGACAG 14
      :|:|||||
RESULT 288
US-09-792-818-344
; Sequence 344, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 344
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-344
      Query Match      1.8%; Score 11; DB 10; Length 17;
      Best Local Similarity 90.9%; Pred. No. 2.3e+05;
      Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      15 GATGAACCGGA 25
      :|:|||||
Db      2 GAUGAACCGGA 12
      :|:|||||
RESULT 289
US-09-792-818-518
; Sequence 518, Application US/09792818

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```
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 707
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-707

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 GATGAACCGGA 25
Db 4 GAUGAACCGGA 14

RESULT 292
US-09-792-818-805
; Sequence 805, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 805
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-805

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 515 TCTCCAGACAG 525
Db 3 UCUCACAGACAG 13

RESULT 293
US-09-792-818-835
; Sequence 835, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 835
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-835
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Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 GATGAACCGGA 25  
Db 1 GAUGAACCGGA 11

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RESULT 294
US-09-745-237A-478
; Sequence 478, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-478
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Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTCGGC 382  
Db 4 GGGGCTCGGC 14

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RESULT 295
US-09-745-237A-1012
; Sequence 1012, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1012
```

Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTCGGC 382  
Db 3 GGGGCTCGGC 13

RESULT 296  
US-09-745-237A-1199  
; Sequence 1199, Application US/09745237A  
; Publication No. US20030143708A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: 400/007 (MBH00-918-A)  
; CURRENT APPLICATION NUMBER: US/09/745,237A  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 4550  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1199  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-745-237A-1199  
Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 372 GGGGCTGCGGC 382  
|||||:||||  
Db 6 GGGGCTGCGGC 16  
RESULT 297  
US-09-745-237A-1533  
; Sequence 1533, Application US/09745237A  
; Publication No. US20030143708A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: 400/007 (MBH00-918-A)  
; CURRENT APPLICATION NUMBER: US/09/745,237A  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 4550  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1533  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-745-237A-1533  
Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 372 GGGGCTGCGGC 382  
|||||:||||  
Db 7 GGGGCTGCGGC 17  
RESULT 298  
US-09-745-237A-1534  
; Sequence 1534, Application US/09745237A  
; Publication No. US20030143708A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: 400/007 (MBH00-918-A)  
; CURRENT APPLICATION NUMBER: US/09/745,237A  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 4550  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1534  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-745-237A-1534  
Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 372 GGGGCTGCGGC 382  
|||||:||||  
Db 1 GGGGCTGCGGC 11  
RESULT 299  
US-09-817-879-345  
; Sequence 345, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 345  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-345  
Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 57 CTGGGCTAAGG 67  
|:|||||  
Db 5 CUGGGCTAAGG 15  
RESULT 300  
US-09-817-879-916  
; Sequence 916, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 916  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-916  
Query Match 1.8%; Score 11; DB 10; Length 17;  
Best Local Similarity 81.8%; Pred. No. 2.3e+05;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGCGGGGCT 386  
|:|||||:  
Db 7 CUGCGGGGCU 17

Search completed: March 5, 2004, 00:28:13  
Job time : 310 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: March 4, 2004, 21:56:12 ; Search time 2279 Seconds  
(without alignments)  
7822.607 Million cell updates/sec

Title: US-09-966-880A-7\_COPY\_80\_676  
Perfect score: 597  
Sequence: 1 atggcagcctcttgatgaa.....ttcgtactttgggactttga 597

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 8854

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vit.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_plg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	1.8	19	9	AI584018 ts12e10.x
2	11	1.8	19	10	AW248934 2819262.3
3	11	1.8	20	28	AZ308068 1M0010N08
4	10	1.7	19	28	AZ308665 1M0011F19

RESULT 1  
AI584018  
LOCUS  
DEFINITION  
ts12e10.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2228394 3', similar to SW:PRPL\_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO 1, mRNA sequence.  
ACCESSION  
AI584018  
VERSION  
AI584018.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

ALIGNMENTS

AI584018 19 bp mRNA linear EST 14-DEC-1999  
ts12e10.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2228394 3', similar to SW:PRPL\_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO 1, mRNA sequence.  
AI584018 GI:4569915  
VERSION  
AI584018.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 3996 Std Error: 0.00  
Seq primer: -40UP from gibco  
High quality sequence stop: 1  
POLYA=No.

Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2228394"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.72 Kb. Life Technologies catalog #:  
11548-013"

ORIGIN  
Query Match 1.8%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGCCGC 222  
Db 6 ACCCTGCCGC 16

RESULT 2  
AW248934 19 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2819262.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819262 3',  
mRNA sequence.  
ACCESSION AW248934  
VERSION AW248934.1 GI:6591927  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819262.5prime  
Contact: Robert Straubeberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCD/DTF cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
PHRED quality bases following vector sequence. Very low  
Quality Sequence: trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence; this cDNA insert was polyadenylated.  
Plate: LLCNI row: C column: 7  
High quality sequence stop: 8.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819262"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"

FEATURES  
source

ORIGIN  
Query Match 1.8%; Score 11; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TTTCGGACTTT 595  
Db 8 TTTCGGACTTT 18

RESULT 3  
AZ308068 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0010N08R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0010N08 R, genomic survey sequence.  
ACCESSION AZ308068  
VERSION AZ308068.1 GI:10347690  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: N column: 08  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0010N08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
http://www.jax.org/resources/documents/dnares/. The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

FEATURES  
source

Insert Length: 3996 Std Error: 0.00  
Seq primer: -40UP from gibco  
High quality sequence stop: 1  
POLYA=No.

Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2228394"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.72 Kb. Life Technologies catalog #:  
11548-013"

ORIGIN  
Query Match 1.8%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGCCGC 222  
Db 6 ACCCTGCCGC 16

RESULT 2  
AW248934 19 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2819262.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819262 3',  
mRNA sequence.  
ACCESSION AW248934  
VERSION AW248934.1 GI:6591927  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819262.5prime  
Contact: Robert Straubeberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCD/DTF cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
PHRED quality bases following vector sequence. Very low  
Quality Sequence: trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence; this cDNA insert was polyadenylated.  
Plate: LLCNI row: C column: 7  
High quality sequence stop: 8.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819262"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"

FEATURES  
source

ORIGIN  
Query Match 1.8%; Score 11; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGCCGC 222  
Db 6 ACCCTGCCGC 16

RESULT 2  
AW248934 19 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2819262.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819262 3',  
mRNA sequence.  
ACCESSION AW248934  
VERSION AW248934.1 GI:6591927  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819262.5prime  
Contact: Robert Straubeberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCD/DTF cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
PHRED quality bases following vector sequence. Very low  
Quality Sequence: trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence; this cDNA insert was polyadenylated.  
Plate: LLCNI row: C column: 7  
High quality sequence stop: 8.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819262"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"

FEATURES  
source



adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.8%; Score 11; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 GCTCTCTCTCC 187

Db |||||

2 GCTCTCTCTCC 12

## RESULT 4

AZ308665

LOCUS

DEFINITION AZ308665 19 bp DNA linear GSS 29-SEP-2000  
clone UUGC1M0011F19 R, genomic survey sequence.

ACCESSION

AZ308665

VERSION

AZ308665.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0011 row: F column: 19

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0011F19"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCC 184

Db |||||

7 TTGCTCTTCC 16

## RESULT 5

AZ790121

LOCUS

DEFINITION AZ790121 19 bp DNA linear GSS 16-FEB-2001  
clone UUGC2M0038P21 F, genomic survey sequence.

ACCESSION

AZ790121

VERSION

AZ790121.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

JOURNAL

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84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: P column: 21

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0038P21"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

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## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 TTTTACTGCT 442  
|||||  
Db 5 TTTTACTGCT 14

## RESULT 6

AZ804026 19 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0064007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0064007 R, genomic survey sequence.

ACCESSION AZ804026  
VERSION AZ804026.1 GI:12956349  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0064 row: 0 column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0064007"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

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## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGGAAC 474  
|||||  
Db 5 TGAAGGAAC 14

## RESULT 7

AZ440002 20 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION 1M0230E19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0230E19 R, genomic survey sequence.

ACCESSION AZ440002  
VERSION AZ440002.1 GI:10564015  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0230 row: E column: 19

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

Location/Qualifiers

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0230E19"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 CATGACCTTC 423  
|||||||  
Db 10 CATGACCTTC 19

## RESULT 8

AZ611227/c  
LOCUS AZ611227 20 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0436E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0436E13 R, genomic survey sequence.

ACCESSION AZ611227  
VERSION AZ611227.1 GI:11733417  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0436 row: E column: 13

Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

source

1..20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0436E13"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 ACCCCAACT 311  
|||||||  
Db 19 ACCCCAACT 10

## RESULT 9

AZ772893  
LOCUS AZ772893 20 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0584D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0584D09 F, genomic survey sequence.

ACCESSION AZ772893  
VERSION AZ772893.1 GI:12896683  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0584 row: D column: 09

Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

source

1..20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0584D09"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 478 AAAGCCTGGG 487  
|||||  
Db 9 AAAGCCTGGG 18

## RESULT 10

AZ815477  
LOCUS  
DEFINITION  
2M0083C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0083C17 R, genomic survey sequence.

ACCESSION  
AZ815477  
VERSION  
AZ815477.1 GI:12985385  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D. Weiss R.

Mouse whole genome scaffolding with paired end reads from 10kb

## plasmid inserts

Unpublished (2000)

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University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0083 row: C column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0083C17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 GTGACAGTGC 116  
|||||  
Db 1 GTGACAGTGC 10

## RESULT 11

AZ964660  
LOCUS  
DEFINITION  
2M0234M21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0234M21 F, genomic survey sequence.

ACCESSION  
AZ964660  
VERSION  
AZ964660.1 GI:13835887  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D. Weiss R.

Mouse whole genome scaffolding with paired end reads from 10kb

## plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0234 row: M column: 21

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0234M21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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## ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCCGACT 289

Db 11 GTGGCCGACT 20

## RESULT 12

CF323895

LOCUS

DEFINITION HDN--05-A22.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA sequence.

ACCESSION

CF323895

VERSION

CF323895.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 10)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..10

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HDN--05-A22"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli SOLR"

/clone\_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 1.5%; Score 9; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 GCCCGAGGG 374

Db 1 GCCCGAGGG 9

## RESULT 13

BH170808/c

LOCUS

DEFINITION SALK\_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_003378, genomic survey sequence.

ACCESSION

BH170808

VERSION

BH170808.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 13)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..13

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_003378"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTTACCGC 332

Db 13 CTTACCGC 5

## RESULT 14

BQ584986

LOCUS

DEFINITION BQ584986 15 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-002-K24-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION

BQ584986

VERSION

BQ584986.1

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, W., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

```

and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 2 row: K column: 24
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:181716"
/db_xref="taxon:161934"
/clone="024-002-K24"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 1.5%; Score 9; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 GAATACCTTT 452
|||||
Db 6 GAATACCTTT 14

RESULT 15
HSM001764
ID HSM001764 standard; mRNA; EST; 16 BP.
XX AC AL037434;
XX SV AL037434.1
XX XX
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX XX
XX DE Homo sapiens mRNA; EST DKFZp564O1471_s1 (from clone DKFZp564O1471)
XX XX
XX KW EST; expressed sequence tag.
XX XX
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX XX
XX RN [1]
XX RP 1-16
XX RA Bloecher H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
XX RT ;
XX RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferstritz 18a D-82152 Martinsried, GERMANY

```

```

XX Clone from S. Wiemann, sequenced by GBF within the cDNA
CC sequencing consortium of the German Genome Project
CC No x1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH Key
FT source
FT 1. .16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp564O1471"
FT /clone_lib="564 (synonym: hibr2). Vector pAMP1; host
FT X1-2blue; sites NotI + Sali"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX SQ Sequence 16 BP; 5 A; 1 C; 0 G; 10 T; 0 other;
Query Match 1.5%; Score 9; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 437
|||||
Db 3 TTATTTT 11

RESULT 16
BQ586219/c
LOCUS
DEFINITION E012392-024-013-C19-SP6-MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-C19 5-PRIME, mRNA sequence.
ACCESSION BQ586219
VERSION BQ586219.1 GI:26115801
KEYWORDS EST.
SOURCE
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 13 row: C column: 19
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186651"
/db_xref="taxon:161934"
/clone="024-013-C19"
/tissue_type="leaf"
/lab_host="EMDH10B"

```

/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCAGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

## ORIGIN

Query Match 1.5%; Score 9; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTTCTTACC 40  
|||||  
DB 13 TTTCTTACC 5

## RESULT 17

CF920788 16 bp mRNA linear EST 05-NOV-2003  
LOCUS gmrhRw3-01 E05 1.039 Soybean root hair subtracted cDNA library  
DEFINITION gmrhRw3 Glycine max cDNA, mRNA sequence.  
ACCESSION CF920788  
VERSION CF920788.1 GI:38191582  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 16)  
AUTHORS Scheffler B.E., Huang, S., Liu X., Nguyen, H., Duke, M. and Stacey, G.  
TITLE Expressed sequence tags from soybean root hair subtractive cDNA library

JOURNAL Unpublished (2003)  
COMMENT Contact: Gary Stacey  
University of Missouri  
108 Waters Hall, Columbia, MO 65211, USA  
Tel: 573-884-4752  
Fax: 573-882-0588  
Email: stacey@missouri.edu  
Single pass sequence  
Seq primer: T7

## FEATURES

source  
1..16  
Location/Qualifiers  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/tissue\_type="root hairs"  
/clone\_lib="Soybean root hair subtracted cDNA library  
gmrhRw3"

/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones  
generated from soybean root hair tissue treated with  
Bradyrhizobium japonicum for 3 hours."

## ORIGIN

Query Match 1.5%; Score 9; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 TCTTCTCC 187  
|||||  
DB 3 TCTTCTCC 11

## RESULT 18

## AZ633696

LOCUS 17 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0489001F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0489001 F, genomic survey sequence.

ACCESSION AZ633696.1 GI:11755886  
VERSION GSS.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: 0 column: 01  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 465.

## FEATURES

source  
1..17  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0489001"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (GI4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 TGGACTTTG 139  
|||||  
DB 4 TGGACTTTG 12

## RESULT 19

```

A1695637
LOCUS       we51q07.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2344668 3'
DEFINITION similar to TR:Q01944 Q01944 EXTENSIN ;contains element MER22
repetitive element ;, mRNA sequence.
ACCESSION  A1695637
VERSION     A1695637.1 GI:4983537
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 19)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgaps-r@mail.nih.gov
           Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
           M.D., Ph.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D.
           CDNA Library Arraying: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1738 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocytic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /notes="Vector: PCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO."

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      485 GGGAGGGC 493
Db      10 GGGAGGGC 18

RESULT 20
LOCUS     AW059909
DEFINITION AUTH.bsst.upc15.ba.A040e11 UPC15 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW059909
VERSION    AW059909.1 GI:5652231
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 19)

A1695637
LOCUS       Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
McCullum,C., Mao,J.I., Kirchner,J.J., Eletz,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
DEFINITION In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
ACCESSION  20144098
VERSION     10677516
KEYWORDS   PUBMED
SOURCE      Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: tim@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the up-regulated gate.
High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocytic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /notes="Vector: PCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO."

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      583 ACTTTGGGA 591
Db      3 ACTTTGGGA 11

RESULT 21
LOCUS     BM399684
DEFINITION 5009-0-60-A01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM399684
VERSION     BM399684.1 GI:18199737
KEYWORDS   EST.
SOURCE      Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT    Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /note="Vector: Bluescript SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)

```



Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 1.5%; Score 9; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 361 GCTGAGCCC 369  
|||||  
Db 2 GCTGAGCCC 10

## RESULT 22

CF276582/c  
LOCUS 19 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--01-M14.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
CF276582  
Oryza sativa cDNA clone 14ETL--01-M14, mRNA sequence.

CF276582.1 GI:33653968

## ACCESSION

CF276582

## KEYWORDS

EST.

## SOURCE

Oryza sativa

## ORGANISM

Oryza sativa

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

## TITLE

Large-scale Sequencing Analysis of Rice ESTs

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
1. .19  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--01-M14"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

## ORIGIN

Query Match 1.5%; Score 9; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 83 ACCTGTGCT 91  
|||||  
Db 18 ACCTGTGCT 10

## RESULT 23

CF309636/c  
LOCUS 19 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-008.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--03-008, mRNA sequence.

## ACCESSION

CF309636

## VERSION

CF309636.1 GI:33691397

## KEYWORDS

EST.

## SOURCE

Oryza sativa

## ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 19)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

## TITLE

Large-scale Sequencing Analysis of Rice ESTs

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1. .19  
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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

## ORIGIN

Query Match 1.5%; Score 9; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 19 ATTCAAAAA 11

## RESULT 24

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LOCUS 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0012E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0012E23 R, genomic survey sequence.

## ACCESSION

AZ309116

## VERSION

AZ309116.1 GI:10349784

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0012 row: E column: 23

Seq primer: CACACAGGAAACAGCTATGACC  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|Gp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES  
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ORIGIN  
Query Match 1.5%; Score 9; DB 28; Length 19;  
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Db 9 TGTAGAAAA 1

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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

453 TGTAGAAAA 461  
|||||  
9 TGTAGAAAA 1

RESULT 26  
AZ323590  
LOCUS  
DEFINITION  
1M0045A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045A07 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|Gp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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ORIGIN  
Query Match 1.5%; Score 9; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
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Qy 338 TCTACTTCT 346  
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Db 11 TCTACTTCT 19

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DEFINITION  
1M0029P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0029P03 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

338 TCTACTTCT 346  
|||||  
11 TCTACTTCT 19

RESULT 25  
AZ312945/c  
LOCUS  
DEFINITION  
1M0029P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0029P03 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Seq primer: CGTTGTAAGAACGACGGCCAGT  
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 High quality sequence stop: 19.  
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 TCGGGCGCAT 536  
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 Db 4 TCGGGCGCAT 12

RESULT 27  
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 LOCUS  
 DEFINITION  
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 clone UUGC1M0054L10 R, genomic survey sequence.

ACCESSION  
 AZ329996  
 VERSION  
 AZ329996.1 GI:10391268  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)

JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0054 row: L column: 10

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCT 442  
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 Db 9 TTTACTGCT 1

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 LOCUS  
 DEFINITION  
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 clone UUGC1M0059M12 R, genomic survey sequence.

ACCESSION  
 AZ331628  
 VERSION  
 AZ331628.1 GI:10394503  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)

JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0059 row: M column: 12

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 Location/Qualifiers  
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## FEATURES

source

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## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
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QY 429 TTATTTT 437  
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 Db 9 TTATTTT 17

RESULT 29  
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 LOCUS  
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 1M007G21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M007G21 R, genomic survey sequence.

ACCESSION  
 AZ344069  
 VERSION  
 AZ344069.1 GI:10422948

KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0077 row: G column: 21

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1. .19

## FEATURES

source

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## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
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QY 302 ACCCCAC 310  
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 Db 3 ACCCCAC 11

RESULT 30  
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LOCUS  
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 1M0080P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0080P01 F, genomic survey sequence.

ACCESSION  
 AZ345537  
 VERSION  
 AZ345537.1 GI:10424774

KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: P column: 01

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 Class: plasmid ends  
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## FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTTATTTTA 437  
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 Db 9 TTTATTTTA 1

## RESULT 31

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 ACCESSION AZ413661  
 VERSION AZ413661.1 GI:10537590  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 TITLE  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0197 row: I column: 07

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0197I07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI\_4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 AAGGGTCGG 72  
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 Db 4 AAGGGTCGG 12

## RESULT 32

AZ424757/c  
 LOCUS AZ424757 19 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0204G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0204G02 R, genomic survey sequence.  
 ACCESSION AZ424757  
 VERSION AZ424757.1 GI:10548770  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0204 row: G column: 02

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0204G02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ACATCCTTT 126  
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 Db 18 ACATCCTTT 10

RESULT 33  
 AZ579566  
 LOCUS 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0367L08P Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0367L08 F, genomic survey sequence.

ACCESSION AZ579566  
 VERSION AZ579566.1 GI:11693995  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: L column: 08

Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0367L08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 547 CTGTATGAG 555  
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 Db 10 CTGTATGAG 18

RESULT 34  
 AZ585367/c

## LOCUS

DEFINITION 1M0390D06R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0390D06 R, genomic survey sequence.

ACCESSION AZ585367  
 VERSION AZ585367.1 GI:11707178  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
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TITLE Unpublished (2000)

## JOURNAL

## COMMENT

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 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0390 row: D column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0390D06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 CATCATGAC 419

Db |||||

9 CATCATGAC 1

## RESULT 35

AZ585898

LOCUS

DEFINITION IM0391L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391L22 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0391 row: L column: 22

Seq primer: CGTTGTAACAGCGGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0391L22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCT 346

Db |||||

6 TCTACTTCT 14

## RESULT 36

AZ593103/c

LOCUS

DEFINITION IM0404N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0404N24 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0404 row: N column: 24

Seq primer: CGTTGTAACAGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /mol\_type="genomic DNA"  
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 /clone="UUGC1M0404N24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 ACGTGGAAAT 175  
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 Db 17 ACGTGGAAAT 9

RESULT 37  
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 LOCUS AZ595016 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION IM0407C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0407C19 F, genomic survey sequence.  
 ACCESSION AZ595016  
 VERSION AZ595016.1 GI:11717206  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
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 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0407 row: C column: 19

Seq primer: CGTTGTAACAGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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# FEATURES

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0407C19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 GAGGGGCTG 378  
 |||||  
 Db 14 GAGGGGCTG 6

RESULT 38  
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 LOCUS AZ595098 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION IM0407E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0407E05 R, genomic survey sequence.  
 ACCESSION AZ595098  
 VERSION AZ595098.1 GI:11717288  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
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 University of Utah  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0407 row: E column: 05



Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0407E05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AAAATGTC 54  
 |||||  
 DB 9 AAAATGTC 1

RESULT 39  
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 LOCUS 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION IM0425E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0425E04 R, genomic survey sequence.  
 ACCESSION AZ604588  
 VERSION AZ604588.1 GI:11726778  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn,D., Ayagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0425 row: E column: 04

Seq primer: CACACAGGAACAGCTATGACC  
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 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
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 /clone="UUGC1M0425E04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAA 49  
 |||||  
 DB 5 AATTCAAA 13

RESULT 40  
 AZ761834/c  
 LOCUS 19 bp DNA linear GSS 16-FEB-2001  
 DEFINITION IM0556E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0556E19 F, genomic survey sequence.  
 ACCESSION AZ761834  
 VERSION AZ761834.1 GI:12871174  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn,D., Ayagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0556 row: E column: 19

Seq primer: CGTTGTAACACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source  
 1. .19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0556E19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CACCGCGCC 396  
 |||||  
 Db 10 CACCGCGCC 2

RESULT 41  
 AZ782026/c  
 LOCUS  
 DEFINITION  
 2M0021123R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0021123 R, genomic survey sequence.

ACCESSION  
 AZ782026  
 VERSION  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rilly,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0021 row: I column: 23

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0021123"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTG 251  
 |||||  
 Db 11 CACCTCCTG 3

RESULT 42  
 AZ865832  
 LOCUS  
 DEFINITION  
 2M0176D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0176D09 F, genomic survey sequence.

ACCESSION  
 AZ865832  
 VERSION  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rilly,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0176 row: D column: 09

Seq primer: CGTTGTAACAGCGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0176D09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

## FEATURES

source

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1. .19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0196J13"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 CTACCTGTG 89  
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 Db 4 CTACCTGTG 12

## RESULT 43

AZ938271/c  
 LOCUS  
 DEFINITION  
 2M0196J13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0196J13 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

## ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Plasmid inserts  
 Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0196 row: J column: 13

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 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 GGCGCATCC 538  
 |||||  
 Db 9 GGCGCATCC 1

## RESULT 44

AB088508

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Mano, H., Noguchi, M., Oshima, T., Yoneyama, T., Hayashi, H. and

Fujiwara, T.

Small RNAs detected in the rice phloem sap

Unpublished (2003)

Contact: Hironori Mano

Plant Genome Center Co., Ltd

Kannondai-25-2, Taikuba, Ibaraki 305-0856, Japan

Tel: 81-298-39-4823

Email: hmano@pgcdna.co.jp

Location/Qualifiers

1. .20

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="PA596"

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/tissue type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 AAAACCATG 466
Db 5 AAAACCATG 13

RESULT 45
AB094447/c
LOCUS
DEFINITION AB094447 lambda Triplex2 rice phloem sap cDNA Oryza sativa
(japonica cultivar-group) cDNA clone PA36, mRNA sequence.
ACCESSION AB094447.1 GI:30307352
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and
Fujiwara,T.
TITLE Small RNAs detected in the rice phloem sap
JOURNAL Unpublished (2003)
COMMENT Contact: Hironori Mano
Plant Genome Center Co.,Ltd
Kannondall-25-2, Tsukuba, Ibaraki 305-0856, Japan
Tel: 81-298-39-4823
Email: hmano@pcdna.co.jp.

FEATURES
source
1..20
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="PA36"
/tissue type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 TCCTCCGCT 190
Db 17 TCCTCCGCT 9

RESULT 46
AU060510
LOCUS
DEFINITION AU060510 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLK222, mRNA sequence.
ACCESSION AU060510.1 GI:4881614
VERSION
KEYWORDS
SOURCE
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostelium discoideum
JOURNAL Unpublished (1998)

```

```

Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES
source
1..20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLK222"
/dev_stage="slug"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATTCAAAA 49
Db 4 AATTCAAAA 12

RESULT 47
AU254527/c
LOCUS
DEFINITION AU254527 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0002395 3', mRNA sequence.
ACCESSION AU254527
VERSION AU254527.1 GI:20316392
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkat@bs.nist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0002395"
/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 TTCAAAAAT 51
Db 19 TTCAAAAAT 11

RESULT 48
BM395007/c

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LOCUS      BM395007      20 bp  mRNA  linear  EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA (large fraction)
ACCESSION  BM395007
VERSION    BM395007.1  GI:18195060
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
REFERENCE  1 (bases 1 to 20)
AUTHORS    Frankel,J.,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J., and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES   Location/Qualifiers
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                        /organism="Tetrahymena thermophila"
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                        /strain="CU428.1"
                        /db_xref="taxon:5911"
                        /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                        /notes="Vector: Bluescript2 SK+; Details on library
                        preparation can be found in Chilcoat and Turkewitz (2001)
                        Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match      1.5%; Score 9; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      160  GGCTGCCAC 168
Db      17  GGCTGCCAC 9

RESULT 49
LOCUS      CF301771      20 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION 7LEAF--06-M03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-M03, mRNA sequence.
ACCESSION  CF301771
VERSION    CF301771.1  GI:33673532
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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                        /organism="Oryza sativa"
                        /mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-M03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
ORIGIN
Query Match      1.5%; Score 9; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      454  GTAGAAAAC 462
Db      12  GTAGAAAAC 20

RESULT 50
LOCUS      D18749/c      20 bp  mRNA  linear  EST 12-DEC-1995
DEFINITION MUSGS01811 Mouse 3'-directed Mus musculus domesticus cDNA clone
            md1693 3', mRNA sequence.
ACCESSION  D18749
VERSION    D18749.1  GI:1100718
KEYWORDS   EST.
SOURCE     Mus musculus domesticus (western European house mouse)
ORGANISM   Mus musculus domesticus
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
TITLE      Analysis of gene expression in mouse embryogenesis by 3'-directed
            cDNA sequencing
JOURNAL    Unpublished (1995)
COMMENT    Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and
            Matsubara,K.
            Institute for Cellular and Molecular Biology
            Osaka University
            3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="Mus musculus domesticus"
                        /mol_type="mRNA"
                        /strain="C57BL/6J"
                        /sub_species="domesticus"
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                        /clone="md1693"
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                        /clone_lib="Mouse 3'-directed"
ORIGIN
Query Match      1.5%; Score 9; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43  TTCAAAAAT 51
Db      19  TTCAAAAAT 11

RESULT 51
LOCUS      AZ339898      20 bp  DNA  linear  GSS 29-SEP-2000
DEFINITION IM0071N04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGCIM0071N04 R, genomic survey sequence.
ACCESSION  AZ339898
VERSION    AZ339898.1  GI:10414624
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0071 row: N column: 04
               Seq primer: CACACAGGAACACAGCTATGACC
               Class: Plasmid ends
               High quality sequence stop: 20.
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               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGCLM0071N04"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGCLM library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [G14732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

FEATURES             source
               1. .20
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               /clone_lib="Mouse 10kb plasmid UUGCLM library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [G14732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

ORIGIN
               Query Match      1.5%; Score 9; DB 28; Length 20;
               Best Local Similarity 100.0%; Pred. No. 1.4e-07;
               Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

               QY      427 GATTATTTT 435
                       |||||
               Db      1 GATTATTTT 9

RESULT 52
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LOCUS      AZ341907      20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION      1M0074F07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0074F07 R, genomic survey sequence.
ACCESSION      AZ341907
VERSION        AZ341907.1      GI:10418624
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

```

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ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0074 row: F column: 07
               Seq primer: CACACAGGAACACAGCTATGACC
               Class: Plasmid ends
               High quality sequence stop: 20.
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               /clone_lib="Mouse 10kb plasmid UUGCLM library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [G14732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

ORIGIN
               Query Match      1.5%; Score 9; DB 28; Length 20;
               Best Local Similarity 100.0%; Pred. No. 1.4e-07;
               Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

               QY      83 ACCTGTGCT 91
                       |||||
               Db      10 ACCTGTGCT 2

RESULT 53
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DEFINITION      1M0082A10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0082A10 F, genomic survey sequence.
ACCESSION      AZ346729
VERSION        AZ346729.1      GI:10425966
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

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ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0082 row: A column: 10  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
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 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [G14732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 CCAACTCTCA 313  
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 Db 9 CCAACTCTCA 17

RESULT 54  
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 LOCUS AZ377958 20 bp DNA linear GSS 02-OCT-2000  
 DEFINITION 1M0132G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0132G02 R, genomic survey sequence.  
 ACCESSION AZ377958  
 VERSION AZ377958.1 GI:10491658  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0132 row: G column: 02  
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 High quality sequence stop: 20.  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [G14732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 CTGGAATAC 449  
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 Db 12 CTGGAATAC 4

RESULT 55  
 AZ429610  
 LOCUS AZ429610 20 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0213H12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0213H12 R, genomic survey sequence.  
 ACCESSION AZ429610  
 VERSION AZ429610.1 GI:10553623  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: H column: 12
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. .20
/organism="Mus musculus"
/mol type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0213H12"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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of pWD42 (G14732114|9b|AF129072.1), a copy-number
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with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred.No.1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CCTCTTGAT 17
Db 11 CCTCTTGAT 19

RESULT 56
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LOCUS
DEFINITION
1X0254M22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0254M22 R, genomic survey sequence.
ACCESSION
AZ453505
VERSION
AZ453505.1 GI:10611371
KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: H column: 12
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Class: plasmid ends
High quality sequence stop: 20.
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/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. .20
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0254M22"
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/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred.No.1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CCTCTTGAT 17
Db 11 CCTCTTGAT 19

RESULT 57
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LOCUS
DEFINITION
1M0302D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0302D18 F, genomic survey sequence.
ACCESSION
AZ480596
VERSION
AZ480596.1 GI:10641661
KEYWORDS
GSS.
Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0254 row: M column: 22
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
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/sex="Male"
/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. .20
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0254M22"
/sex="Male"
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/clone lib="Mouse 10kb plasmid UUGC1M library"
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred.No.1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 GCATGAAAA 503
Db 16 GCATGAAAA 8

RESULT 57
AZ480596
LOCUS
DEFINITION
1M0302D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0302D18 F, genomic survey sequence.
ACCESSION
AZ480596
VERSION
AZ480596.1 GI:10641661
KEYWORDS
GSS.
Mus musculus (house mouse)

```



ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0302 row: D column: 18  
 Seq primer: CTTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0302D18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FWP42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTC 183

Db 1 TTGCTCTTC 9

## RESULT 58

AZ482160  
 LOCUS AZ482160 20 bp DNA linear GSS 04-OCT-2000  
 DEFINITION IM0307G09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0307G09 F, genomic survey sequence.  
 ACCESSION AZ482160  
 VERSION AZ482160.1 GI:10643225  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0307 row: G column: 09  
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 High quality sequence stop: 20.  
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 /clone="UUGC1M0307G09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FWP42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 GGCTGCACC 391

Db 9 GGCTGCACC 17

## RESULT 59

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 LOCUS AZ486306 20 bp DNA linear GSS 05-OCT-2000  
 DEFINITION IM0314B13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0314B13 F, genomic survey sequence.  
 ACCESSION AZ486306  
 VERSION AZ486306.1 GI:10652951  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0314 row: B column: 13
Seq primer: CATTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/clone="UUGC1M0314B13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 GCTACCGCG 232
Db 18 GCTACCGCG 10

RESULT 60
AZ504441
LOCUS
DEFINITION
1M0344F15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0344F15 R, genomic survey sequence.
ACCESSION
AZ504441
VERSION
AZ504441.1 GI:10685757
KEYWORDS
GSS.
Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0344 row: F column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 AAATTCAGT 509
Db 4 AAATTCAGT 12

RESULT 61
AZ591658
LOCUS
DEFINITION
1M0401F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0401F19 R, genomic survey sequence.
ACCESSION
AZ591658
VERSION
AZ591658.1 GI:11713848
KEYWORDS
GSS.
Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0401 row: F column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 CTGCTGAA 446
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Db 1 CTGCTGAA 9

RESULT 62
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LOCUS
DEFINITION
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IM0419H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0419H15 R, genomic survey sequence.
ACCESSION
AZ601483
VERSION
AZ601483.1 GI:11723673
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0401 row: F column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M041F19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and 14
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 CTGCTGAA 446
|||||
Db 1 CTGCTGAA 9

RESULT 62
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LOCUS
DEFINITION
20 bp DNA linear GSS 13-DEC-2000
IM0419H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0419H15 R, genomic survey sequence.
ACCESSION
AZ601483
VERSION
AZ601483.1 GI:11723673
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0419 row: H column: 15
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Class: plasmid ends
High quality sequence stop: 20.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0419H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and 14
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 ACTGTGCC 274
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Db 12 ACTGTGCC 4

RESULT 63
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LOCUS
DEFINITION
20 bp DNA linear GSS 13-DEC-2000
IM0463D01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0463D01 R, genomic survey sequence.
ACCESSION
AZ624669
VERSION
AZ624669.1 GI:11746859
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

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ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0463 row: D column: 01
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES      source
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0463D01"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnates/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (G1[4732114]gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 TTGTAGAA 459
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      7 TTGTAGAA 15

RESULT 64
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LOCUS      AZ651194      20 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION IM0521F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0521F18 R, genomic survey sequence.
ACCESSION  AZ651194
VERSION     AZ651194.1 GI:11786441
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0521 row: F column: 18
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0521F18"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnates/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (G1[4732114]gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAAC 309
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      11 AACCCCAAC 3

RESULT 65
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LOCUS      AZ653361      20 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION IM0527D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0527D04 F, genomic survey sequence.
ACCESSION  AZ653361
VERSION     AZ653361.1 GI:11790507
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0527 row: D column: 04
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              High quality sequence stop: 20.
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              /sex="Male"
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              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

FEATURES      source
              1. .20
              /organism="Mus musculus"
              /mol_type="genomic DNA"
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              /clone="UUGC1M0527D04"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
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              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 CAAAAATGT 53
Db      20 CAAAAATGT 12

RESULT 66
LOCUS      AZ655977/c
DEFINITION 1M0531E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0531E13 F, genomic survey sequence.
ACCESSION  AZ655977
VERSION     AZ655977.1 GI:11793123
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0531 row: E column: 13
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              Class: plasmid ends
              High quality sequence stop: 20.
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              /strain="C57BL/6J"
              /db_xref="taxon:10090"
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              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      296 GAGGGAACC 304
Db      9 GAGGGAACC 1

RESULT 67
LOCUS      AZ656648
DEFINITION 1M0532P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0532P16 F, genomic survey sequence.
ACCESSION  AZ656648
VERSION     AZ656648.1 GI:11793794
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0532 row: P column: 16  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

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/clone="UUGC1M0532P16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 GGAAGGGGCT 494

Db 5 GGAAGGGGCT 13

RESULT 68  
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DEFINITION 2M0009L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0009L24 F, genomic survey sequence.  
ACCESSION AZ776071  
VERSION AZ776071.1 GI:12903267  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: L column: 24  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

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/db\_xref="taxon:10090"  
/clone="UUGC2M0009L24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

source

1..20  
/organism="Mus musculus"  
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musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
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adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 GAAGGGGCTG 495

Db 11 GAAGGGGCTG 19

RESULT 69  
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LOCUS AZ780925 20 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0018A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0018A16 R, genomic survey sequence.  
ACCESSION AZ780925  
VERSION AZ780925.1 GI:12913099  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0018 row: A column: 16  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
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/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 312 CAGCTCTGAG 320  
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DB 8 CAGCTCTGAG 16  
RESULT 70  
AZ820009  
LOCUS AZ820009  
DEFINITION 2M0091P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0091P23 R, genomic survey sequence.  
ACCESSION AZ820009  
VERSION AZ820009.1 GI:12989917  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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University of Utah  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0091 row: P column: 23  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
FEATURES  
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1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0091P23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 401 TGCAATAG 409  
|||||||  
DB 11 TGCAATAG 19  
RESULT 71  
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LOCUS AZ822878  
DEFINITION 2M0096E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0096E02 R, genomic survey sequence.  
ACCESSION AZ822878  
VERSION AZ822878.1 GI:12992786  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 401 TGCAATAG 409  
|||||||  
DB 11 TGCAATAG 19  
RESULT 71  
AZ822878  
LOCUS AZ822878  
DEFINITION 2M0096E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0096E02 R, genomic survey sequence.  
ACCESSION AZ822878  
VERSION AZ822878.1 GI:12992786  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: E column: 02  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source

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1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096202"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 CCGCGCGCG 398  
|||||  
Db 6 CCGCGCGCG 14

RESULT 72  
AZ833695/c  
LOCUS  
DEFINITION 2M0115N20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC2M0115N20 R, genomic survey sequence.  
ACCESSION AZ833695  
VERSION AZ833695.1 GI:13003603  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0115 row: N column: 20  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source

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1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0115N20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCG 380  
|||||  
Db 10 GGGGCTGCG 2

RESULT 73  
TA207B03Q  
LOCUS  
DEFINITION TA207B03Q 20 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 207b03, reverse sequence,  
genomic survey sequence.  
ACCESSION AL475823  
VERSION AL475823.1 GI:11842591  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei



```

ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
Location/Qualifiers
1..20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="207b03"
ORIGIN
Query Match 1.5%; Score 9; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 492 GCTGCATGA 500
|||||
Db 8 GCTGCATGA 16

RESULT 74
CF313731/c
LOCUS
DEFINITION
HD--01-P12.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
ACCESSION
CF313731
VERSION
CF313731.1 GI:33685492
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 8)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivat="Nackdong"
/db_xref="taxon:4530"

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/clone="HD--01-P12"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli DH10B"
/clone.lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOP0; Site_1: EcoRI; Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.7e+09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 AARACCAT 465
|||||
Db 8 AARACCAT 1

RESULT 75
BG925375
LOCUS
DEFINITION
HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG925375
VERSION
BG925375.1 GI:14319898
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL
Osteoarthritis Cartilage cDNA libraries
MEDLINE
21482651
PUBMED
11597177
COMMENT
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: T7.
FEATURES
source
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab host="E.coli DH10 B"
/clone.lib="HNC (Human Normal Cartilage)"
/notes="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 CGCATCCT 539
|||||
Db 3 CGCATCCT 10

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RESULT 76
BQ585171
LOCUS
DEFINITION
  S014222-024-001-J02-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
  CNA clone 024-001-J02-5-PRIME, mRNA sequence.
ACCESSION
  BQ585171
VERSION
  BQ585171.1 GI:26114753
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 11)
  Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
MEDLINE
  22362189
PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 11 Std Error: 0.00
  Plate: 1 row; J column; 02
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES
  source
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    Location/Qualifiers
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS320 (double haploid, monogerm breeding
    line)"
    /db_xref="GABI:181534"
    /db_xref="taxon:161934"
    /clone="024-001-J02"
    /tissue_type="inflorescence"
    /lab_host="EMDH108"
    /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
    cDNA library from sugar beet, library provided by KWS
    Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
    orientation:
    SP6-Sali-CCGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
  Query Match 1.3%; Score 8; DB 13; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 457 GAAACCA 464
  Db 1 GAAACCA 8
  |||||
  |||||

RESULT 77
CF300559/c
LOCUS
DEFINITION
  7LEAF--05-B09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION
  CF300559
VERSION
  CF300559.1 GI:33672320
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 11)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
TITLE
  Contact: Nahm B.H.
JOURNAL
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
COMMENT
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
  1..11
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--05-B09"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 429 TTATTTT 436
  Db 9 TTATTTT 2
  |||||
  |||||

RESULT 78
BH213431/c
LOCUS
DEFINITION
  BH213431 Arabidopsis thaliana TDNA insertion lines Arabidopsis
  thaliana genomic clone SALK_009214, genomic survey sequence.
ACCESSION
  BH213431
VERSION
  BH213431.1 GI:16395344
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 11)
  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
  Shinn,P., Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished (2001)
TITLE
  Contact: Joseph R. Ecker
JOURNAL
  Salk Institute Genomic Analysis Laboratory (SIGNAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA.
  Class: TDNA tagged.
  Location/Qualifiers
  1..11
  /organism="Arabidopsis thaliana"
  /mol_type="genomic DNA"
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  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 429 TTATTTT 436
  Db 9 TTATTTT 2
  |||||
  |||||

RESULT 79
BH213431/c
LOCUS
DEFINITION
  BH213431 Arabidopsis thaliana TDNA insertion lines Arabidopsis
  thaliana genomic clone SALK_009214, genomic survey sequence.
ACCESSION
  BH213431
VERSION
  BH213431.1 GI:16395344
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 11)
  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
  Shinn,P., Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished (2001)
TITLE
  Contact: Joseph R. Ecker
JOURNAL
  Salk Institute Genomic Analysis Laboratory (SIGNAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA.
  Class: TDNA tagged.
  Location/Qualifiers
  1..11
  /organism="Arabidopsis thaliana"
  /mol_type="genomic DNA"
  /clone="SALK_009214"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 429 TTATTTT 436
  Db 9 TTATTTT 2
  |||||
  |||||

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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GALK 009214"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497
|||||
Db 11 GGGCTGCA 4

RESULT 79
BG925521/c
LOCUS BG925521 12 bp mRNA linear EST 06-NOV-2001
DEFINITION HNC3-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG925521
VERSION BG925521.1 GI:14320044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
source 1..12
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGAAGGG 492
|||||
Db 8 GGAAGGG 1

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GALK 009214"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497
|||||
Db 11 GGGCTGCA 4

RESULT 79
BG925521/c
LOCUS BG925521 12 bp mRNA linear EST 06-NOV-2001
DEFINITION HNC3-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG925521
VERSION BG925521.1 GI:14320044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
source 1..12
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGAAGGG 492
|||||
Db 8 GGAAGGG 1

```

```

RESULT 80
CF280439
LOCUS CF280439 12 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-B21.bi Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-B21, mRNA sequence.
ACCESSION CF280439
VERSION CF280439.1 GI:33657825
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
source 1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--07-B21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 CCTTCAA 426
|||||
Db 3 CCTTCAA 10

CF311969
LOCUS CF311969 12 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-H13, mRNA sequence.
ACCESSION CF311969
VERSION CF311969.1 GI:33683730
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1. .12

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF-07-H13"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.3e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CGTGACAG 113

Db 9 CGTGACAG 2

## RESULT 82

CF329021/c

LOCUS CF329021 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-D03.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-D03, mRNA sequence.

ACCESSION CF329021

VERSION CF329021.1 GI:33806279

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1. .12

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--04-D03"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.3e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTT 435

Db 10 ATTATTTT 3

## RESULT 83

BG927437

LOCUS BG927437 13 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC1-1-H7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG927437

VERSION BG927437.1 GI:14321960

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 13)

AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sache, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lark, M.W.

TITLE Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL 21482651

MEDLINE 11597177

PUBMED

COMMENT

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7.

## FEATURES

source

1. .13

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI;  
Directional"

## ORIGIN

Query Match 1.3%; Score 8; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.4e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 CTTTCTGC 295

Db 3 CTTTCTGC 10

## RESULT 84

BQ582420

LOCUS BQ582420 13 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012207-024-001-J02-SP6 MP12-ADIS-024-Inflorcescence Beta vulgaris cDNA clone 024-001-J02 5-PRIME, mRNA sequence.

ACCESSION BQ582420

VERSION BQ582420.1 GI:26111997

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

```

REFERENCE
AUTHORS      1 (bases 1 to 13)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radloff,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 13 Std Error: 0.00
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              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
source       1..13
              Location/Qualifiers
              ..13
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:181155"
              /db_xref="taxon:161934"
              /clone="024-001-J02"
              /tissue_type="inflorescence"
              /lab_host="EMDH10B"
              /clone_lib="MPIZ-ADIS-024-inflorescence"
              /note="Vector: pCMVSPORT6; Site 1: Sali; site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      457 GAAACCA 464
        |||||
        1 GAAACCA 8

RESULT 85
BQ595423/c
LOCUS      BQ595423
DEFINITION E012693-024-022-N20-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-N20 5-PRIME, mRNA sequence.
ACCESSION  BQ595423
VERSION     BQ595423.1 GI:26125006
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 13)
AUTHORS      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radloff,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698

```

```

COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 13 Std Error: 0.00
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              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
source       1..13
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              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:191428"
              /db_xref="taxon:161934"
              /clone="024-022-N20"
              /tissue_type="developing root"
              /lab_host="EMDH10B"
              /clone_lib="MPIZ-ADIS-024-developing root"
              /note="Vector: pCMVSPORT6; Site 1: Sali; site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 GTGGAATT 176
        |||||
        11 GTGGAATT 4

RESULT 86
CF291168/c
LOCUS      CF291168
DEFINITION 14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION  CF291168
VERSION     CF291168.1 GI:33660201
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE        Contact: Nahm B.H.
JOURNAL      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnaahm@gbio.com, bnaahm@bio.myongji.ac.kr.
FEATURES
source       1..13
              Location/Qualifiers
              ..13
              /organism="Oryza sativa"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:4530"

```

CONTACT: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel. 773.702.4224  
Fax. 773.702.4224

CONTACT: LUKNEWICZ AF  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

# FEATURES

Location/Qualifiers

1. .14  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 1.3%; Score 8; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368  
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DB 5 GCTGAGCC 12

## RESULT 90

BQ589337/c  
LOCUS BQ589337 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION S014007-024-015-002-SP6 MP12-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-015-002 5-PRIME, mRNA sequence.

ACCESSION BQ589337.1 GI:26118920  
VERSION BQ589337  
KEYWORDS EST.

## ORGANISM

Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE  
PUBMED 22362189

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de  
Insert length: 14 Std Error: 0.00

Plate: 15 row: 0 column: 02

Seq primer: SP6; CATACGATTAGTGACACTATAG.

## FEATURES

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/mol\_type="mRNA"  
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/db\_xref="GABI:187733"  
/db\_xref="taxon:161934"  
/clone="024-015-002"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

## ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTCTCTT 37  
|||||  
DB 9 GTTCTCTT 2

## RESULT 91

CA853334/c  
LOCUS CA853334 14 bp mRNA linear EST 01-AUG-2003  
DEFINITION B07A06.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone  
B07A06 5', mRNA sequence.

ACCESSION CA853334  
VERSION CA853334.1 GI:33390127  
KEYWORDS EST.

## SOURCE

Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 14)  
Alkharouf, N.W., Khan, R. and Matthews, B.F.

TITLE Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
Unpublished (2002)  
JOURNAL CONTACT: Alkharouf, N.W.  
COMMENT Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

## FEATURES

source

1. .14  
Location/Qualifiers  
/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Peking"

/db\_xref="taxon:3847"

/clone="B07A06"

/tissue\_type="Roots"

/dev\_stage="Seedlings"

/clone\_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA

extracted from roots of soybean cv. Peking 12 hrs after

infection by SCN race 3. These are cloned in pBluescript

SK- phagemid."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTT 182  
|||||  
DB 11 TTGCTCTT 4

## RESULT 92

CF301021/c  
LOCUS CF301021 14 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library 11 (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301021

VERSION CF301021.1 GI:33672782

```

KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

ORIGIN
Query Match          1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
Db 9 TTATTTT 2

RESULT 93
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LOCUS        BF219911
DEFINITION   BF219911 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:2961653 3',
            mRNA sequence.
ACCESSION    BF219911
VERSION      BF219911
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 15)
            /note="NIH-MGC http://mgc.nci.nih.gov/"
            /clone_lib="National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)"
            /contact="Robert Strausberg, Ph.D.
            Email: cgabsp@remail.nih.gov
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloned and sequenced by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRAL1 row: n column: 20
            High quality sequence stop: 5.

FEATURES
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KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
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                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

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Query Match          1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
Db 9 TTATTTT 2

RESULT 93
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LOCUS        BF219911
DEFINITION   BF219911 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:2961653 3',
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ACCESSION    BF219911
VERSION      BF219911
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 15)
            /note="NIH-MGC http://mgc.nci.nih.gov/"
            /clone_lib="National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)"
            /contact="Robert Strausberg, Ph.D.
            Email: cgabsp@remail.nih.gov
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloned and sequenced by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            High quality sequence stop: 5.

FEATURES
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KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

ORIGIN
Query Match          1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
Db 9 TTATTTT 2

RESULT 93
BF219911
LOCUS        BF219911
DEFINITION   BF219911 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:2961653 3',
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ACCESSION    BF219911
VERSION      BF219911
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 15)
            /note="NIH-MGC http://mgc.nci.nih.gov/"
            /clone_lib="National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)"
            /contact="Robert Strausberg, Ph.D.
            Email: cgabsp@remail.nih.gov
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloned and sequenced by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRAL1 row: n column: 20
            High quality sequence stop: 5.

FEATURES
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                /mol_type="mRNA"
                /db_xref="taxon:9606"

KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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                /cultivar="Nackdong"
                /db_xref="taxon:4530"
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                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

ORIGIN
Query Match          1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
Db 9 TTATTTT 2

RESULT 93
BF219911
LOCUS        BF219911
DEFINITION   BF219911 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:2961653 3',
            mRNA sequence.
ACCESSION    BF219911
VERSION      BF219911
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            1 (bases 1 to 15)
            /note="NIH-MGC http://mgc.nci.nih.gov/"
            /clone_lib="National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)"
            /contact="Robert Strausberg, Ph.D.
            Email: cgabsp@remail.nih.gov
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloned and sequenced by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRAL1 row: n column: 20
            High quality sequence stop: 5.

FEATURES
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                /organism="Homo sapiens"
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KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr
```



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ACCESSION      BQ594980
VERSION        BQ594980.1  GI:26124563
KEYWORDS       EST.
SOURCE         Beta vulgaris
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Caryophyllales; Amaranthaceae; Beta.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
               Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
               and Radelof,U.
TITLE          Construction of a 'unigene' cDNA clone set by oligonucleotide
               fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL        Plant J. 32 (5), 845-857 (2002)
MEDLINE        22362189
PUBMED         12472698
COMMENT        Contact: Weishaar B
               ADIS DNA core facility at MPIZ
               Max-Planck-Institute for Plant Breeding Research
               Carl-von-Linne Weg 10, 50829 Koeln, Germany
               Fax: 00492215062851
               Email: weishaar@piz-koeln.mpg.de
               Insert Length: 15 Std Error: 0.00
               Row: 23 column: 24
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES       Location/Qualifiers
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               /db_xref="taxon:161934"
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               /lab_host="EMDH10B"
               /clone_lib="MP1Z-ADIS-024-developing root"
               /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
               cDNA library from sugar beet, library provided by KWS
               Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
               b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGGCTCG-5prime-cDNA-polYA-CC-NotI-r7; Note:
               Sequencing granted in the context of the GABI-Beet
               project, local PI: Dr. Katharina Schneider, coordinator:
               Prof. Christian Jung; Sequence submission managed by
               RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
Db 6 TTTTACT 13

RESULT 96
CA796369
LOCUS          CA796369
DEFINITION    15 bp mRNA linear EST 05-DEC-2002
               Cac BL_3383 Cac BL (Bean and Leaf from Amelonado type Cacao)
               Theobroma cacao cDNA clone Cac_BL_3383 5', mRNA sequence.
ACCESSION     CA796369
VERSION       CA796369.1  GI:26053445
KEYWORDS      EST.
SOURCE        Theobroma cacao (cacao)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;

CDNA clone 024-023-J24 5-PRIME, mRNA sequence.
BQ594980
BQ594980.1  GI:26124563
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Row: 23 column: 24
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES       Location/Qualifiers
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               /cultivar="KWS2320 (double haploid, monogerm breeding
               line)"
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               /db_xref="taxon:161934"
               /clone="024-023-J24"
               /tissue_type="developing root"
               /lab_host="EMDH10B"
               /clone_lib="MP1Z-ADIS-024-developing root"
               /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
               cDNA library from sugar beet, library provided by KWS
               Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
               b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGGCTCG-5prime-cDNA-polYA-CC-NotI-r7; Note:
               Sequencing granted in the context of the GABI-Beet
               project, local PI: Dr. Katharina Schneider, coordinator:
               Prof. Christian Jung; Sequence submission managed by
               RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
Db 6 TTTTACT 13

RESULT 96
CA796369
LOCUS          CA796369
DEFINITION    15 bp mRNA linear EST 05-DEC-2002
               Cac BL_3383 Cac BL (Bean and Leaf from Amelonado type Cacao)
               Theobroma cacao cDNA clone Cac_BL_3383 5', mRNA sequence.
ACCESSION     CA796369
VERSION       CA796369.1  GI:26053445
KEYWORDS      EST.
SOURCE        Theobroma cacao (cacao)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;

Theobroma.
1 (bases 1 to 15)
Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES       Location/Qualifiers
               source            1..15
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               /mol_type="mRNA"
               /strain="Amelonado type"
               /db_xref="taxon:3641"
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               /cell_type="Whole organ"
               /dev_stage="maturity"
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               /clone_lib="Cac BL (Bean and Leaf from Amelonado type
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ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 348 TGAGGACC 355
Db 3 TGAGGACC 10

RESULT 97
CF290849/c
LOCUS          CF290849
DEFINITION    15 bp mRNA linear EST 14-AUG-2003
               14ROOT--01-A17-G1 Rice root plasmid cDNA library (14ROOT) Oryza
               sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION     CF290849
VERSION       CF290849.1  GI:33659882
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
               Large-scale Sequencing Analysis of Rice ESTs
               Unpublished (2003)
JOURNAL        Contact: Nahm B.H.
COMMENT        Genomics and Genetics Institute, Greengene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.
FEATURES       Location/Qualifiers
               source            1..15
               /organism="Oryza sativa"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:4530"
               /clone="14ROOT--01-A17"

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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
DB 8 TTATTTT 1

RESULT 98
CF291030/c      15 bp mRNA linear EST 14-AUG-2003
LOCUS          sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
DEFINITION     CF291030
ACCESSION      CF291030
VERSION        CF291030.1 GI:33660063
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-E19"
/tissue_type="root"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
DB 10 TTATTTT 3

RESULT 99
CF316846      15 bp mRNA linear EST 15-AUG-2003
LOCUS          HP--06-F02-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION     library (HD) Oryza sativa cDNA clone HD--06-F02, mRNA sequence.


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ACCESSION      CF316846
VERSION        CF316846.1 GI:33688607
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-F02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96
DB 2 GCTACGTA 9

RESULT 100
AA881100
LOCUS          16 bp mRNA linear EST 26-MAR-1998
DEFINITION     v206d08.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1314927.5' Similar to SW:UBCI_HUMAN P50550
UBIQUITIN-CONJUGATING ENZYME E2-18 KD ; mRNA sequence.
ACCESSION      AA881100
VERSION        AA881100.1 GI:2990410
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE          The WashU-HHMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108


```

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:685223

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

#### FEATURES

source

FEATURES  
source

1. .16  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1314927"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NbMMG"  
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.7e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTCTCTCC 187  
|||||  
Db 10 CTCTCTCC 3

#### RESULT 102

AA937877

LOCUS

DEFINITION

AA937877 16 bp mRNA linear EST 30-APR-1998  
NW90606.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1253890  
similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ; mRNA  
sequence.

ACCESSION AA937877.1 GI:3095988

VERSION AA937877

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,

Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

#### FEATURES

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:685223

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

#### FEATURES

source

1. .16  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1314927"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NbMMG"  
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.7e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30  
|||||  
Db 3 GGAGGAAG 10

#### RESULT 101

AA881100/c

LOCUS

DEFINITION

AA881100 16 bp mRNA linear EST 26-MAR-1998  
VZ06d08.r1 Soares mammary gland NbMMG Mus musculus cDNA clone  
IMAGE:1314927 5' similar to SW:UBCI HUMAN P50550  
UBIQUITIN-CONJUGATING ENZYME E2-18 KD ; mRNA sequence.

ACCESSION AA881100.1 GI:2990410

VERSION AA881100

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 16)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Waterson, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterson, R.

Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

```

source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1253890"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr12"
/note="Vector: PAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN
Query Match 1.3%; Score 8; DB 9; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
|||||
Db 9 TTATTTT 16

RESULT 103
BG926060
LOCUS
DEFINITION HNC23-1-E1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG926060
VERSION BG926060.1 GI:14320583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteocarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar@lsgsk.com
Seq primer: T7.

FEATURES
source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCTTCCT 185
|||||

source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCTTCCT 185
|||||

```

```

Db 5 CTCCTCCT 12

RESULT 104
CF920788
LOCUS
DEFINITION smrrw3-01_E05_1_039 Soybean root hair subtracted cDNA library
smrrw3 Glycine max cDNA, mRNA sequence.
ACCESSION CF920788
VERSION CF920788.1 GI:38191582
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schaffner,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
TITLE Expressed sequence tags from soybean root hair subtractive cDNA
library
JOURNAL Unpublished (2003)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: stacey@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES
source
1. .16
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
smrrw3"
/note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30
|||||
Db 11 GGAGGAAG 4

RESULT 105
AW247673
LOCUS
DEFINITION AW247673
AW247673.1 GI:6590666
ACCESSION AW247673
VERSION AW247673.1 GI:6590666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESRs: 2820207.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue procurement: DCTD/DTP cDNA Library Preparation: Ling

```

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image.html](http://www.bio.llnl.gov/bbrp/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.

Plate: L1CM3 row: J column: 16.

#### FEATURES

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2820207"

/issue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.7e+07; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 366 GCCCGAGG 373  
|||||||

Db 2 GCCCGAGG 9

#### RESULT 106

AW247949  
LOCUS AW247949 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 282605.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820605 3', mRNA sequence.  
ACCESSION AW247949  
VERSION AW247949.1 GI:6591037  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2820605.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTP/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image.html](http://www.bio.llnl.gov/bbrp/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM4 row: K column: 6.

#### FEATURES

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2820605"

/issue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.7e+07; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

Qy 432 TTTTACT 439  
|||||||

Db 6 TTTTACT 13

#### RESULT 107

AW251033/c  
LOCUS AW251033 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821399.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821399 3', mRNA sequence.  
ACCESSION AW251033  
VERSION AW251033.1 GI:6593979  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821399.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTP/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image.html](http://www.bio.llnl.gov/bbrp/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM6 row: L column: 8

High quality sequence stop: 17.

## FEATURES

## Location/Qualifiers

```

1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821399"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

```

Query Match      1.3%; Score 8; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      43  TTTCAAAA 50
         |||||
DB       13  TTTCAAAA 6
```

## RESULT 108

## BM399748

## LOCUS

## DEFINITION

5009-0-60-H02.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..17

## /organism="Tetrahymena thermophila"

## /mol\_type="mRNA"

## /strain="CU428.1"

## /db\_xref="taxon:5911"

## /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

## /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## 8; Conservative

## 0; Mismatches

## 0; Indels

## 0; Gaps

## 0;

## QY

## 326

## TCACCGCG

## 333

## |||||

## DB

## 8

## TCACCGCG

## 15

## RESULT 109

## BQ591588

## LOCUS

## DEFINITION

CDNA clone 024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

EST.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## 1..17

## /organism="Beta vulgaris"

## /mol\_type="mRNA"

## /cultivar="XWS2320 (double haploid, monogerm breeding line)"

## /db\_xref="GABI:188532"

## /db\_xref="taxon:161934"

## /clone="024-017-C15"

## /tissue\_type="storage root"

## /lab\_host="EMDH10B"

## /clone\_lib="MP1Z-ADIS-024-storage root"

## /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"

## SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## 8; Conservative

## 0; Mismatches

## 0; Indels

## 0; Gaps

## 0;

## QY

## 429

## TTATTTT

## 436

## |||||

## DB

## 1

## TTATTTT

## 8

## RESULT 110

## CA797283

## LOCUS

## DEFINITION

Cac\_BL\_4376 Cac.BL (Bean and Leaf from Amelonardo type Cacao)

Theobroma cacao cDNA clone Cac\_BL\_4376 5', mRNA sequence.

## ACCESSION

## VERSION

## 110

## QY

## 326

## TCACCGCG

## 333

## |||||

## DB

## 8

## TCACCGCG

## 15

## RESULT 111

## CA797283

## LOCUS

## DEFINITION

Cac\_BL\_4376 Cac.BL (Bean and Leaf from Amelonardo type Cacao)

Theobroma cacao cDNA clone Cac\_BL\_4376 5', mRNA sequence.

## ACCESSION

## VERSION

## 111

## QY

## 326

## TCACCGCG

## 333

## |||||

## DB

## 8

## TCACCGCG

## 15

Email: Paul.Jones@eu.affm.com  
 Seq primer: T3.

FEATURES  
 source  
 1. .17  
 Location/Qualifiers  
 /organism="Theobroma cacao"  
 /mol\_type="rRNA"  
 /strain="Amelonado type"  
 /db\_xref="taxon:3641"  
 /clone="Cac BL 4642"  
 /tissue\_type="Mature leaf and mature bean"  
 /cell\_type="Whole organ"  
 /dev\_stage="maturity"  
 /lab\_host="XL-1 Blue MRF"  
 /clone\_lib="Cac\_BL (Bean and Leaf from Amelonado type Cacao)"  
 /notes="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."

ORIGIN  
 Query Match 1.3%; Score 8; DB 14; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 409 GCCATCAT 416  
 |||||  
 Db 13 GCCATCAT 6

RESULT 112  
 CF299737/c  
 LOCUS  
 DEFINITION  
 7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-N22, mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1. (bases 1 to 17)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .17  
 Location/Qualifiers  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--03-N22"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /notes="Vector: pCR4-TOPO; Site1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN  
 Query Match 1.3%; Score 8; DB 14; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      46 AAAATGTT 53
Db      15 AAAATGTT 8

RESULT 113
CF310268      17 bp mRNA linear EST 15-AUG-2003
DEFINITION   ABF--04-N06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--04-N06, mRNA sequence.
ACCESSION    CF310268
KEYWORDS     CF310268.1 GI:33682029
SOURCE       EST.
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
              1..17
              /organism="Oryza sativa"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:4530"
              /clone="ABF--04-N06"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="ABF3-overexpressing transgenic rice plasmid
              cDNA library (ABF)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
              for 2hrs. Oligo-capped mRNA was reverse transcribed and
              then used for PCR. mRNA was prepared from ABA-responsive
              element binding transcription factor 3 overexpression
              line."
ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      129 ACTGGACT 136
Db      8 ACTGGACT 15

PCH303755      17 bp DNA linear GSS 03-APR-2001
DEFINITION   Plasmodium chabaudi genome survey sequence, clone PC7C5.plt,
              genomic survey sequence.
ACCESSION    AJ303755
VERSION      AJ303755.1 GI:11140262
KEYWORDS     GSS; genome survey sequence.
SOURCE       Plasmodium chabaudi
              Plasmodium chabaudi
              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
              Bowman,S., Phillips,R.S. and Turner,C.M.
              Gene discovery in Plasmodium chabaudi by genome survey sequencing
              TITLE

```

---

```

JOURNAL      Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE      21192558
PUBMED       11295179
REFERENCE    2 (bases 1 to 17)
AUTHORS      Janssen,C.S.
TITLE        Direct Submission
JOURNAL      Submitted (06-NOV-2000) Division of Infection & Immunity,
              University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
COMMENT      bases 39 to 55 (QL to SR).
FEATURES     Location/Qualifiers
              1..17
              /organism="Plasmodium chabaudi"
              /mol_type="genomic DNA"
              /db_xref="taxon:5825"
              /clone="PC7C5.plt"
ORIGIN
Query Match      1.3%; Score 8; DB 29; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      430 TATTTTGA 437
Db      6 TATTTTGA 13

RESULT 115
AW246505      18 bp mRNA linear EST 07-JAN-2000
LOCUS        2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
DEFINITION   mRNA sequence.
ACCESSION    AW246505
VERSION      AW246505.1 GI:65899498
KEYWORDS     EST.
SOURCE       Homo sapiens
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORIGIN        1 (bases 1 to 18)
              NIH-MGC http://mgi.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Other ESTs: 2821585.5prime
              Contact: Robert Strausberg, Ph.D.
              Email: cgabs@rmail.nih.gov
              Tissue Procurement: DCTD/DP cDNA Library Preparation: Ling
              Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
              Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
              project Clone distribution: MGC clone distribution information can
              be found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
              Scores: PHRED from University of Washington Genome Center. Vector
              Trimming: cross_match from University of Washington Genome Center
              PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
              Drosophila Genome Project. University of Washington Genome Center:
              http://www.genome.washington.edu/Low Quality Sequence: 18
              contiguous PHRED high quality bases following vector sequence. Very
              Low Quality Sequence: trace file contained 18 contiguous distinct
              peaks following vector sequence. Polyadenylation: Based upon the
              presence of a XhoI site followed by a run of 14 or more T residues
              at the beginning of the sequence, this cDNA insert was
              polyadenylated.
              Plate: L1CM7 row: D column: 2
              High quality sequence stop: 18.
              Location/Qualifiers
              1..18
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:2821585"
              /tissue_type="small cell carcinoma"
              /cell_line="MGC3"
              /lab_host="DH10B (phage-resistant)"
              source

```



```

/clone lib="NIH_MGC 7"
/Note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

## ORIGIN

```

Query Match      1.3%; Score 8; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 31 TTTCTTTA 38
      |||||
Db 8 TTTCTTTA 15

```

## RESULT 116

```

BG927414
LOCUS      18 bp mRNA linear EST 06-NOV-2001
DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

```

```

ACCESSION   BG927414
VERSION     BG927414.1 GI:14321937
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

```

```

REFERENCE   1 (bases 1 to 18)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathie, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.

```

```

TITLE       Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL     Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE     21482651
PUBMED      11597177

```

```

COMMENT     Contact: Sanjay Kumar
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay.kumar-1@sk.com
            Seq primer: T7.

```

## FEATURES

```

source
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/Note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

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## ORIGIN

```

Query Match      1.3%; Score 8; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 513 TCTCTCCA 520
      |||||
Db 9 TCTCTCCA 16

```

## RESULT 117

```

BG395336

```

```

LOCUS      BM395336      18 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-8-F05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM395336
VERSION     BM395336.1 GI:18195389
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila

```

```

REFERENCE   1 (bases 1 to 18)
AUTHORS    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.

```

```

TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

```

## FEATURES

```

source
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/Note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

```

## ORIGIN

```

Query Match      1.3%; Score 8; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 198 GGACTGGG 205
      |||||
Db 1 GGACTGGG 8

```

## RESULT 118

```

BG395686

```

```

LOCUS      BM395686      18 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-10-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM395686
VERSION     BM395686.1 GI:18195739
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila

```

```

REFERENCE   1 (bases 1 to 18)
AUTHORS    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.

```

```

TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

```

## FEATURES

```

source
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"

```

REFERENCE	Eukaryota, Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
AUTHORS	1 (bases 1 to 18) Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu Seq primer: T3.
FEATURES	Location/Qualifiers 1..18 /organism="Tetrahymena thermophila" /mol_type="mRNA" /strain="CU428.1" /db_xref="taxon:5911" /clone_lib="Chilcoat"/Turkewitz cDNA (large fraction)" /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN	Query Match 1.3%; Score 8; DB 12; Length 18; Best Local Similarity 100.0%; Pred. No. 4,8e+07; Indels 0; Gaps 0; Matches 8; Conservative 0; Mismatches 0; QY 326 TCACCGCG 333 DB 4 TCACCGCG 11 
RESULT 121	18 bp mRNA linear EST 17-JAN-2002
BM400623	5009-0-76-F06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
LOCUS	Tetrahymena thermophila cDNA, mRNA sequence.
DEFINITION	BM400623
ACCESSION	BM400623.1 GI:18200676
VERSION	EST.
KEYWORDS	Tetrahymena thermophila
SOURCE	Tetrahymena thermophila
ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu Seq primer: T3.
FEATURES	Location/Qualifiers 1..18 /organism="Tetrahymena thermophila" /mol_type="mRNA" /strain="CU428.1" /db_xref="taxon:5911" /clone_lib="Chilcoat"/Turkewitz cDNA (large fraction)" /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN	

Query Match 1.3%; Score 8; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 TCACCGCG 333  
 |||||  
 Db 5 TCACCGCG 12

RESULT 122  
 BQ584794/c  
 LOCUS  
 DEFINITION BQ584794 18 bp mRNA linear EST 06-DEC-2002  
 cDNA clone 024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris  
 ACCESSION BQ584794  
 VERSION BQ584794.1 GI:26114371  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radloff,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 18 Std Error: 0.00  
 Plate: 2 row: E column: 13  
 Seq primer: SP6r; ATTAGGTGACACTATAGAGA.  
 Location/Qualifiers  
 1..18  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:181907"  
 /db\_xref="taxon:161934"  
 /clone="024-002-E13"  
 /tissue\_type="inflorescence"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-inflorescence"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Query Match 1.3%; Score 8; DB 13; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 AACCCCAA 308  
 |||||  
 Db 17 AACCCCAA 10

RESULT 124  
 BQ591606  
 LOCUS  
 DEFINITION BQ591606 18 bp mRNA linear EST 06-DEC-2002  
 cDNA clone 024-017-G11-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 ACCESSION BQ591606  
 VERSION BQ591606.1 GI:26121189  
 KEYWORDS EST.  
 SOURCE Beta vulgaris

RESULT 123  
 BQ586069  
 LOCUS  
 DEFINITION BQ586069 18 bp mRNA linear EST 06-DEC-2002  
 cDNA clone 024-013-B09-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 ACCESSION BQ586069  
 VERSION BQ586069.1 GI:26115651  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radloff,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 18 Std Error: 0.00  
 Plate: 13 row: B column: 09  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
 Location/Qualifiers  
 1..18  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:186792"  
 /db\_xref="taxon:161934"  
 /clone="024-013-B09"  
 /tissue\_type="leaf"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-leaf"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Query Match 1.3%; Score 8; DB 13; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CAAAAATG 52  
 |||||  
 Db 8 CAAAAATG 15

RESULT 124  
 BQ591606  
 LOCUS  
 DEFINITION BQ591606 18 bp mRNA linear EST 06-DEC-2002  
 cDNA clone 024-017-G11-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 ACCESSION BQ591606  
 VERSION BQ591606.1 GI:26121189  
 KEYWORDS EST.  
 SOURCE Beta vulgaris

```

ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS      Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.
and Radolof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Email: weishaar@piz-koeln.mpg.de
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Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 TTTTCACT 131
Db 4 TTTTCACT 11

RESULT 125
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LOCUS      HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION
sequence.
ACCESSION  C00629
VERSION     C00629.1 GI:1432859
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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Qy 321 GATCTTCA 328
Db 4 GATCTTCA 328

RESULT 126
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DEFINITION
sequence.
ACCESSION  C21365
VERSION     C21365.1 GI:1622475
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 126
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LOCUS      HUMGS0005154 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION  C21365
VERSION     C21365.1 GI:1622475
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 457 GAAACCA 464
Db 10 GAAACCA 17

```

```

Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
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sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
FEATURES
Location/Qualifiers
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Qy 457 GAAACCA 464
Db 10 GAAACCA 17

RESULT 126
C21365
LOCUS      HUMGS0005154 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION  C21365
VERSION     C21365.1 GI:1622475
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
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since 1993. For the abundance information of clones with this
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sequences of the clones represented by this GS sequences is also
found there.
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 GATCTTCA 328
Db 4 GATCTTCA 328

RESULT 125
C00629
LOCUS      HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION
sequence.
ACCESSION  C00629
VERSION     C00629.1 GI:1432859
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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Qy 457 GAAACCA 464
Db 10 GAAACCA 17

RESULT 126
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DEFINITION
sequence.
ACCESSION  C21365
VERSION     C21365.1 GI:1622475
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo,K.
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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Db 10 GAAACCA 17

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ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 11 TTTTACT 18

RESULT 130
CF310639
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-G10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-G10, mRNA sequence.
ACCESSION  CF310639
VERSION     CF310639.1 GI:33682400
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 18)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            derived from rice Histone Deacetylase overexpression
            line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
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QY 89 GCTACGTA 96
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DB 2 GCTACGTA 9

RESULT 132
CF314887
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--03-J15.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION  CF314887
VERSION     CF314887.1 GI:33686648
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 18)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
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            line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
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QY 89 GCTACGTA 96
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DB 2 GCTACGTA 9

RESULT 131
CF314452
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-P15.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-P15, mRNA sequence.
ACCESSION  CF314452
VERSION     CF314452.1 GI:33686213
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE  1 (bases 1 to 18)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
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Db 7 TTTTACT 14

RESULT 133
CF329020
LOCUS
DEFINITION
NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION
CF329020
VERSION
CF329020.1 GI:33806277
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..18
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/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
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Db 7 TTTTACT 14

RESULT 133
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LOCUS
DEFINITION
NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION
CF329020
VERSION
CF329020.1 GI:33806277
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
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Db 7 TTTTACT 14

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Db 10 TTTTACT 17

RESULT 134
CF329484
LOCUS
DEFINITION
NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION
CF329484
VERSION
CF329484.1 GI:33807207
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..18
source
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
|||||
Db 11 TTTTACT 18

RESULT 135
CF329485/c
LOCUS
DEFINITION
NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION
CF329485
VERSION
CF329485.1 GI:33807209
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

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/organism="Oryza sativa"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439

Db 8 TTTTACT 1

## RESULT 136

CF332520

LOCUS

DEFINITION JMT--01-A23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa CDNA clone JMT--01-A23, mRNA sequence.

ACCESSION

CF332520

VERSION

CF332520.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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/organism="Oryza sativa"  
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/cultivar="Nackdong"  
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## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96

Db 2 GCTACGTA 9

## RESULT 137

CF333354

LOCUS

DEFINITION JMT--02-D13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa CDNA clone JMT--02-D13, mRNA sequence.

ACCESSION

CF333354

VERSION

CF333354.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"  
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## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96

Db 2 GCTACGTA 9

## RESULT 138

CF334471

LOCUS

DEFINITION JMT--03-M11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa CDNA clone JMT--03-M11, mRNA sequence.

ACCESSION

CF334471

VERSION

CF334471.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



REFERENCE  
 AUTHORS Ehrhartoidae; Oryzae; Oryza.  
 1 (bases 1 to 18)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongwi University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongwi.ac.kr.

## FEATURES

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 /lab\_host="E.coli DH10B"  
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 cDNA library (JMT)"  
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## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 QY 89 GCTACGTA 96  
 |||||  
 Db 2 GCTACGTA 9

## RESULT 139

D11849  
 LOCUS HUMEM02G05 Liver HepG2 cell line. Homo sapiens cDNA clone hm02g05,  
 mRNA sequence.  
 D11849 18 bp mRNA linear EST 02-DEC-1992  
 DEFINITION  
 ACCESSION D11849.1 GI:2155112  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 18)  
 Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.  
 and Matsubara, K.

TITLE Large scale cDNA sequencing for analysis of quantitative and  
 qualitative aspects of gene expression  
 JOURNAL Nat. Genet. 2, 173-179 (1992)  
 MEDLINE 94258199  
 PUBMED 1345164

CONTACT: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki  
 Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 1-3 Yamada-oka, Suita, Osaka 565, Japan.

## FEATURES

source  
 1..18  
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ORIGIN  
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 /note="3'-directed regional cDNA library. Cleaved by MboI  
 and transformed into E.coli."

Query Match 1.3%; Score 8; DB 14; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 QY 120 ATCCTTTT 127  
 |||||  
 Db 2 ATCCTTTT 9

RESULT 140  
 BZ424455/c  
 LOCUS BZ424455 18 bp DNA linear GSS 13-DEC-2002  
 DEFINITION 10012978-5039 Aspergillus terreus random genomic DNA clone library  
 Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424455  
 VERSION BZ424455.1 GI:26665910  
 KEYWORDS GSS.

SOURCE Aspergillus terreus  
 ORGANISM Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 1 (bases 1 to 18)  
 Askew, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,  
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
 Madden, K.T.

TITLE Integrating transcriptional and metabolite profiles to direct the  
 engineering of lovastatin-producing strains

JOURNAL Unpublished (2002)  
 COMMENT Contact: Zimmer DP  
 Microbia, Inc.  
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-

Email: dzimmer@microbia.com  
 Class: plasmid ends.

## FEATURES

source  
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 /organism="Aspergillus terreus"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"  
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 pZExOTM-2"

## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 155 AGACGGC 162  
 |||||  
 Db 8 AGACGGC 1

## RESULT 141

BZ424583/c  
 LOCUS BZ424583 18 bp DNA linear GSS 13-DEC-2002  
 DEFINITION 10015692-4695 Aspergillus terreus random genomic DNA clone library  
 Aspergillus terreus genomic, genomic survey sequence.  
 ACCESSION BZ424583  
 VERSION BZ424583.1 GI:26666038  
 KEYWORDS GSS.

SOURCE Aspergillus terreus  
 ORGANISM Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,  
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
 Madden, K.T.  
 TITLE Integrating transcriptional and metabolite profiles to direct the  
 engineering of lovastatin-producing strains  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Zimmer DP  
 Microbia, Inc.  
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
 Class: plasmid ends.  
 Location/Qualifiers  
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 /db\_xref="taxon:33178"  
 /lab\_host="Escherichia coli"  
 /clone\_lib="Aspergillus terreus random genomic DNA clone  
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 /note="Vector: pZBrOTM-2; Site 1: Sau3A; Site 2: BamHI;  
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 pZBrOTM-2"

FEATURES  
source

RESULT 142  
 BZ424682/C  
 LOCUS 18 bp DNA linear GSS 13-DEC-2002  
 DEFINITION 100017874-4841 Aspergillus terreus random genomic DNA clone library  
 Aspergillus terreus genomic, genomic survey sequence.  
 ACCESSION BZ424682  
 VERSION BZ424682.1 GI:26666137  
 KEYWORDS GSS.  
 SOURCE Aspergillus terreus  
 ORGANISM Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,  
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
 Madden, K.T.  
 TITLE Integrating transcriptional and metabolite profiles to direct the  
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 JOURNAL Unpublished (2002)  
 COMMENT Contact: Zimmer DP  
 Microbia, Inc.  
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
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## ORIGIN

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 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162  
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 DB 8 AGAACGGC 1

RESULT 142  
 BZ424682/C  
 LOCUS 18 bp DNA linear GSS 13-DEC-2002  
 DEFINITION 100017874-4841 Aspergillus terreus random genomic DNA clone library  
 Aspergillus terreus genomic, genomic survey sequence.  
 ACCESSION BZ424682  
 VERSION BZ424682.1 GI:26666137  
 KEYWORDS GSS.  
 SOURCE Aspergillus terreus  
 ORGANISM Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,  
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
 Madden, K.T.  
 TITLE Integrating transcriptional and metabolite profiles to direct the  
 engineering of lovastatin-producing strains  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Zimmer DP  
 Microbia, Inc.  
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
 Class: plasmid ends.  
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 /organism="Aspergillus terreus"  
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 pZBrOTM-2"

/organism="Aspergillus terreus"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"  
 /db\_xref="taxon:33178"  
 /lab\_host="Escherichia coli"  
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Query Match 1.3%; Score 8; DB 28; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162  
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 DB 8 AGAACGGC 1

RESULT 143  
BZ424714/C

LOCUS 18 bp DNA linear GSS 13-DEC-2002  
 DEFINITION 100018520-2995 Aspergillus terreus random genomic DNA clone library  
 Aspergillus terreus genomic, genomic survey sequence.  
 ACCESSION BZ424714  
 VERSION BZ424714.1 GI:26666169  
 KEYWORDS GSS.  
 SOURCE Aspergillus terreus  
 ORGANISM Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,  
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
 Madden, K.T.  
 TITLE Integrating transcriptional and metabolite profiles to direct the  
 engineering of lovastatin-producing strains  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Zimmer DP  
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 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
 Class: plasmid ends.  
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 /note="Vector: pZBrOTM-2; Site 1: Sau3A; Site 2: BamHI;  
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 pZBrOTM-2"

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162  
 |||||  
 DB 8 AGAACGGC 1

FEATURES  
 source  
 1..18  
 Location/Qualifiers

One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
 Class: plasmid ends.

FEATURES  
 source  
 1. .18  
 Location/Qualifiers  
 /organism="Aspergillus terreus"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"  
 /db\_xref="taxon:33178"  
 /lab\_host="Escherichia coli"  
 /clone\_lib="Aspergillus terreus random genomic DNA clone library"  
 /note="Vector: pZEROTM-2; Site.1: Sau3A; Site.2: BamHI; Sau3A genomic fragments ligated into BamHI digested pZEROTM-2"

ORIGIN  
 Query Match 1.3%; Score 8; DB 28; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAAGCGC 162  
 |||  
 Db 8 AGAAGCGC 1

RESULT 146  
 BZ424914/c

LOCUS  
 BZ424914 18 bp DNA linear GSS 13-DEC-2002

DEFINITION  
 100021302-5049 Aspergillus terreus random genomic DNA clone library

ACCESSION  
 BZ424914 Aspergillus terreus genomic, genomic survey sequence.

VERSION  
 BZ424914.1 GI:26666369

KEYWORDS  
 GSS.

SOURCE  
 Aspergillus terreus

ORGANISM  
 Aspergillus terreus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 1 (bases 1 to 18)

REFERENCE  
 1 Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,  
 Zimmer,D.P., Boers,M.-B., Blomquist,P.R., Martinez,E.J.,  
 Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,  
 Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and  
 Madden,K.T.

AUTHORS  
 Integrating transcriptional and metabolite profiles to direct the  
 engineering of lovastatin-producing strains

TITLE  
 Unpublished (2002)

JOURNAL  
 Contact: Zimmer DP

COMMENT  
 Microbia, Inc.  
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA  
 Tel: 617-621-8322  
 Fax: 617-  
 Email: dzimmer@microbia.com  
 Class: plasmid ends.

FEATURES  
 source  
 1. .18  
 Location/Qualifiers  
 /organism="Aspergillus terreus"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"  
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 /lab\_host="Escherichia coli"  
 /clone\_lib="Aspergillus terreus random genomic DNA clone library"  
 /note="Vector: pZEROTM-2; Site.1: Sau3A; Site.2: BamHI; Sau3A genomic fragments ligated into BamHI digested pZEROTM-2"

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 Query Match 1.3%; Score 8; DB 28; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Sa3A genomic fragments ligated into BamHI digested
pZerOTM-2 "

ORIGIN
Query Match      1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
|||||
Db 8 AGAACGGC 1

RESULT 150
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LOCUS      18 bp DNA linear GSS 13-DEC-2002
DEFINITION 100029638-4999 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION  BZ425326
VERSION    BZ425326.1 GI:26666781
KEYWORDS   GSS..
SOURCE     Aspergillus terreus
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
            Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
            Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
            Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
            Madden,K.T.
TITLE     Integrating transcriptional and metabolite profiles to direct the
            engineering of lovastatin-producing strains
JOURNAL   Unpublished (2002)
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            Microbia, Inc.
            One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
            Tel: 617-621-8322
            Fax: 617-
            Email: dzimmer@microbia.com
            Class: plasmid ends.

FEATURES             source
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
|||||
Db 8 AGAACGGC 1

RESULT 152
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LOCUS      18 bp DNA linear GSS 13-DEC-2002
DEFINITION 100032032-5025 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION  BZ425442
VERSION    BZ425442.1 GI:26666897
KEYWORDS   GSS.
SOURCE     Aspergillus terreus
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
            Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
            Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
            Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
            Madden,K.T.
TITLE     Integrating transcriptional and metabolite profiles to direct the
            engineering of lovastatin-producing strains
JOURNAL   Unpublished (2002)
COMMENT   Contact: Zimmer DP
            Microbia, Inc.
            One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
            Tel: 617-621-8322
            Fax: 617-
            Email: dzimmer@microbia.com
            Class: plasmid ends.

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            /organism="Aspergillus terreus"
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            /strain="ATCC 20542 (A. terreus Thom, anamorph)"
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
|||||
Db 8 AGAACGGC 1

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DEFINITION 100031360-4855 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION  BZ425405
VERSION    BZ425405.1 GI:26666860
KEYWORDS   GSS.
SOURCE     Aspergillus terreus

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Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 18)
AUTHORS   Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
            Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
            Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
            Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
            Madden,K.T.
TITLE     Integrating transcriptional and metabolite profiles to direct the
            engineering of lovastatin-producing strains
JOURNAL   Unpublished (2002)
COMMENT   Contact: Zimmer DP
            Microbia, Inc.
            One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
            Tel: 617-621-8322
            Fax: 617-
            Email: dzimmer@microbia.com
            Class: plasmid ends.

FEATURES             source
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            /mol_type="genomic DNA"
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            /lab_host="Escherichia coli"
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
|||||
Db 8 AGAACGGC 1

RESULT 152
BZ425442/c
LOCUS      18 bp DNA linear GSS 13-DEC-2002
DEFINITION 100032032-5025 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION  BZ425442
VERSION    BZ425442.1 GI:26666897
KEYWORDS   GSS.
SOURCE     Aspergillus terreus
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
            Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
            Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
            Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
            Madden,K.T.
TITLE     Integrating transcriptional and metabolite profiles to direct the
            engineering of lovastatin-producing strains
JOURNAL   Unpublished (2002)
COMMENT   Contact: Zimmer DP
            Microbia, Inc.
            One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
            Tel: 617-621-8322
            Fax: 617-
            Email: dzimmer@microbia.com
            Class: plasmid ends.

FEATURES             source
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            /organism="Aspergillus terreus"

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/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
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/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/notes="Vector: pZEROM-2; Site_1: Sau3A; Site_2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZEROM-2"

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAAGCGC 162
    |||||
Db 8 AGAAGCGC 1

RESULT 153
HSM007596 standard; mRNA; EST; 19 BP.
XX
AC AL042746;
SV AL042746.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434C1822_r1 (from clone DKFZp434C1822)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
XX 1-19
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MLPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
XX sequencing consortium of the German Genome Project
XX No s1 sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX source
XX 1. 19
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XX /mol_type="mRNA"
XX /organism="Homo sapiens"
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XX /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX DH10B; sites NotI + SalI"
XX /dev_stage="adult"
XX /tissue_type="testis"
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XX Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;
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XX Query Match      1.3%; Score 8; DB 2; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+07;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 CGCGCCGG 398
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Db 1 CGCGCCGG 8

RESULT 154
AA884867 19 bp mRNA linear EST 04-JAN-1999
LOCUS am21b11.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1467453 3' similar to TR:Q93040 Q93040 TIF1BETA ZINC FINGER
PROTEIN. [1] ; mRNA sequence.
ACCESSION AA884867
VERSION AA884867.1 GI:2994848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 19
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/clone_lib="Soares NFL T GBC S1"
/notes="Organ: pooled; Vector: p77T3D-Pac (Pharmacia) with
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Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      1.3%; Score 8; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CGTGACAG 113
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Db 4 CGTGACAG 11

RESULT 155
AA885697 19 bp mRNA linear EST 09-JUN-1998
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DEFINITION similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPFI. [1] ; mRNA
sequence.
ACCESSION AA885697
VERSION AA885697.1 GI:3000805
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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/note="Organ: lung; Vector: p77T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p77T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES  
source

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AATAGCCA 412  
Db 1 AATAGCCA 8  
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RESULT 156  
AA928295/c  
LOCUS  
DEFINITION  
AA928295  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295 19 bp mRNA linear EST 22-APR-1998  
O160107.s1 NCI\_CGAP\_HN4 Homo sapiens cDNA clone IMAGE:1487077 3' similar to TR:Q14244 Q14244 MICROTUBULE ASSOCIATED PROTEIN. 7, mRNA sequence.  
AA928295  
AA928295.1 GI:3077451  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI/MIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Dental Research,

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AATAGCCA 412  
Db 1 AATAGCCA 8  
|||||

RESULT 156  
AA928295/c  
LOCUS  
DEFINITION  
AA928295  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295 19 bp mRNA linear EST 22-APR-1998  
O160107.s1 NCI\_CGAP\_HN4 Homo sapiens cDNA clone IMAGE:1487077 3' similar to TR:Q14244 Q14244 MICROTUBULE ASSOCIATED PROTEIN. 7, mRNA sequence.  
AA928295  
AA928295.1 GI:3077451  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI/MIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Dental Research,

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295/c  
LOCUS  
DEFINITION  
AA928295  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295 19 bp mRNA linear EST 22-APR-1998  
O160107.s1 NCI\_CGAP\_HN4 Homo sapiens cDNA clone IMAGE:1487077 3' similar to TR:Q14244 Q14244 MICROTUBULE ASSOCIATED PROTEIN. 7, mRNA sequence.  
AA928295  
AA928295.1 GI:3077451  
EST.  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI/MIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Dental Research,

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295/c  
LOCUS  
DEFINITION  
AA928295  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AA928295 19 bp mRNA linear EST 22-APR-1998  
O160107.s1 NCI\_CGAP\_HN4 Homo sapiens cDNA clone IMAGE:1487077 3' similar to TR:Q14244 Q14244 MICROTUBULE ASSOCIATED PROTEIN. 7, mRNA sequence.  
AA928295  
AA928295.1 GI:3077451  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI/MIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Dental Research,

JOURNAL  
COMMENT

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: John Ensley, M.D.  
cDNA Library Preparation: Stratagene, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1487077"  
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/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="NCI CGAP HN4"  
/note="Organ: pharynx; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' (GA)10ACTAGTCGAGTTTTTTTTTTTTTTT 3' "

FEATURES  
source

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
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RESULT 157  
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LOCUS  
DEFINITION  
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AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
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Query Match 1.3%; Score 8; DB 9; Length 19;  
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
|||||

RESULT 157  
AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
|||||

RESULT 157  
AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
|||||

RESULT 157  
AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
|||||

RESULT 157  
AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261  
Db 18 GCCCCTGC 11  
|||||

RESULT 157  
AI017940  
LOCUS  
DEFINITION  
AI017940 19 bp mRNA linear EST 27-AUG-1998  
cu24b04.x1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627183 3' similar to SW:MB4C DROME Q01644 MALE SPECIFIC SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.  
AI017940  
AI017940.1 GI:3232276  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 1853 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1627183"

/lab\_host="DH10B"  
 /clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
 /notes="Organ: pooled; Vector: pTVT3-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NbHPU, testis NHT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. Clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaudo."

## ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 GACCGCAA 359

Db 1 GACCGCAA 8

## RESULT 158

AI122861 19 bp mRNA linear EST 03-SEP-1998  
 LOCUS q01c07.s1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
 DEFINITION IMAGE:1694988 3' similar to SW:DGK\_HUMAN Q16854 DEOXYGUANOSINE  
 KINASE PRECURSOR ; mRNA sequence.

ACCESSION AI122861

VERSION AI122861.1 GI:3538627

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pTVT3-Pac; Site\_1: Not I;

Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pTVT3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaudo."

## ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.9e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 47 AAAATGTC 54  
 |||||  
 Db 4 AAAATGTC 11

## RESULT 159

AI122861/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pTVT3-Pac; Site\_1: Not I;

Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pTVT3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaudo."

## ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 160

AI1476315

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pTVT3-Pac; Site\_1: Not I;

Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pTVT3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaudo."



```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Trace considered overall poor quality
Insert Length: 502 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES
    source
        1..19
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:204144"
        /tissue_type="follicular lymphoma"
        /lab_host="NCI CGAP_lym5"
        /clone_lib="NCI CGAP_lym5"
        /notes="Organ: lymph node; Vector: pBluescript SK-; Site: 1:
        EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
        Oligo dt. Average insert size 1.2 kb. Non-amplified
        library. -5' adaptor sequence: 5' GAATTCGACGAG 3' -3'
        adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
ORIGIN
    Query Match      1.3%; Score 8; DB 9; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4.9e+07;
    Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      213 CCTCGGCC 220
        |||||
Db      4 CCTCGGCC 11

RESULT 161
AI524591
LOCUS      AI524591.1 19 bp mRNA linear EST 12-MAY-1999
DEFINITION      t043f09.x1 NCI CGAP U4 Homo sapiens CDNA clone IMAGE:2181833 3'
                similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 4 ; mRNA sequence.
ACCESSION      AI524591
VERSION      AI524591.1 GI:4438726
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Trace considered overall poor quality
Insert Length: 1117 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES
    source
        1..19
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:224943"
        /tissue_type="adenocarcinoma"
        /lab_host="DH10B"
        /clone_lib="NCI CGAP_Pan1"
        /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: SalI;
        Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        found through the I.M.A.G.E. Consortium/LLNL at:
        www-bio.llnl.gov/bbrp/image/image.html
JOURNAL
    COMMENT      Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html

```

```

Trace considered overall poor quality
Insert Length: 502 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES
    Location/Qualifiers
        1..19
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2181833"
        /tissue_type="serous papillary carcinoma, high grade, 2
        pooled tumors"
        /lab_host="DH10B"
        /clone_lib="NCI CGAP_Ut-4"
        /note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1: SalI;
        Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 1.48 kb. Life Technologies catalog #:
        11542-016"
ORIGIN
    Query Match      1.3%; Score 8; DB 9; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4.9e+07;
    Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      264 CGACTGTG 271
        |||||
Db      3 CGACTGTG 10

RESULT 162
AI569191/c
LOCUS      AI569191.1 19 bp mRNA linear EST 14-MAY-1999
DEFINITION      t-r3f12.x1 NCI CGAP Pan1 Homo sapiens CDNA clone IMAGE:2224943 3'
                similar to SW:PRCE_HUMAN P28074 PROTEASOME EPSILON CHAIN PRECURSOR
                mRNA sequence.
ACCESSION      AI569191
VERSION      AI569191.1 GI:4532565
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Trace considered overall poor quality
Insert Length: 1117 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES
    Location/Qualifiers
        1..19
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2224943"
        /tissue_type="adenocarcinoma"
        /lab_host="DH10B"
        /clone_lib="NCI CGAP_Pan1"
        /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: SalI;
        Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        found through the I.M.A.G.E. Consortium/LLNL at:
        www-bio.llnl.gov/bbrp/image/image.html
JOURNAL
    COMMENT      Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www-bio.llnl.gov/bbrp/image/image.html

```

Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

## ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 213 CCTGGCC 220

Db 8 CCTGGCC 1

## RESULT 163

AI641650

LOCUS

DEFINITION

AI641650 19 bp mRNA linear EST 07-JUN-2001  
fc22a01.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone  
IMAGE:3722088 3' similar to TR:Q93107 Q93107 MYOSIN I HEAVY CHAIN  
KINASE. ; contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS

1 (bases 1 to 19)  
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
Eddy, S., Hillier, D., Kucaba, T., Martin, J., Beck, C., Wyllie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Bitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.

TITLE

JOURNAL

COMMENT

WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: zbrfish@wustl.edu  
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: www.genomesystems.com) (email contact:  
info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
(web address: www.regen.com) (email contact: info@regen.com) and  
ReSourceZentrumPrimarDatenbank, Berlin, Germany (web address:  
www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: T7 ET from AmerSham

High quality sequence stop: 1.

## FEATURES

source

1..19  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3722088"  
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/tissue\_type="26 somite embryos, adult livers, shield  
stage embryos"  
/lab\_host="XLI-blue MRF"  
/clone\_lib="Zebrafish WashU MPIMG EST"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st  
strand cDNA was primed with a Not I - oligo (dT)15 primer  
[5'-GACTAGTCTTAGTCGAGCGCGCCCTTTTCTTTTCTTTT3'];  
double-stranded cDNA was ligated to Sal I adaptors (BRL),  
digested with Not I and cloned into the Not I and Sal I  
sites of the pSPORT1 vector (BRL). Library was constructed  
by Matthew Clark (Lehrach lab, ICRF, London and Max Planck  
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST

analysis were selected following oligonucleotide  
hybridization fingerprinting of arrayed clones from  
zebrafish late somitogenesis (26 ss), adult liver or  
embryonic shield stage (5.6 h) libraries. Fingerprint  
data were used to computationally cluster cDNAs, and a  
single cDNA from each cluster was chosen for sequencing.  
In some cases multiple members of the same cluster were  
sequenced to assess clustering parameters or single clones  
were sequenced additional times to assess quality  
control."

## ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 301 AACCCCAA 308

Db 12 AACCCCAA 19

## RESULT 164

AI683556

LOCUS

DEFINITION

AI683556 19 bp mRNA linear EST 16-DEC-1999  
tx67h08.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2274687 3',  
similar to TR:Q24099 Q24099 MTN12 ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1385 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2274687"

/tissue\_type="well-differentiated endometrial

adenocarcinoma, 7 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Utl1"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.75 kb. Life Technologies catalog #:

11538-014"

## ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

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Qy 243 CACCTCCT 250
Db 12 CACCTCCT 19

RESULT 165
AW063940/c
LOCUS
DEFINITION
  DP0975 KRIIB Human DP intrathymic T-cell cDNA library Homo sapiens
  CDNA 3', mRNA sequence.
ACCESSION
  AW063940
VERSION
  AW063940.1 GI:8887877
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C.,
  Park,J.-H., Kim,Y.-S. and Lee,C.-C.
TITLE
  Gene expression profile and identification of differentially
  expressed transcripts during human intrathymic T-cell development
  by cDNA sequencing analysis
JOURNAL
  Genomics 70 (1), 1-18 (2000)
MEDLINE
  20541704
PUBMED
  11087656
COMMENT
  Contact: Sung-Ho Goh
  Genome Center
  Korea Research Institute of Bioscience and Biotechnology
  Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea
  Tel: 82-42-860-4473
  Fax: 82-42-860-4479
  Email: gohsh@mail.kribb.re.kr
  Seq primer: T7
  High quality sequence stop: 15
  POLYA=No.

FEATURES
    source
    1..19
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2821119"
    /tissue_type="small cell carcinoma"
    /cell_line="MGC3"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_7"
    /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
    EcoRI; cDNA made by oligo-dT priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Size-selected >500bp for average
    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
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1 (bases 1 to 19)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821119.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

1 (bases 1 to 19)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PRAP suite. Poly-T identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu/LowQualitySequence>. Very Low  
PHRED high quality bases following vector sequence. 7 contiguous  
Quality Sequence: Trace file contained 19 contiguous distinct peaks  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LHCMS row: P column: 16  
High quality sequence stop: 7.

1..19  
Location/Qualifiers  
source  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821119"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.3%; Score 8; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436  
Db 9 TTATTTT 16

RESULT 167  
AW248820/c  
LOCUS  
DEFINITION  
 AW248820.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821008 3',  
 mRNA sequence.  
ACCESSION  
 AW248820  
VERSION  
 AW248820.1 GI:6591813  
KEYWORDS  
 EST.  
SOURCE  
 Homo sapiens (human)  
ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
 1 (bases 1 to 19)  
AUTHORS  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 Other ESTs: 2821008.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

1.3%; Score 8; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TTCTGTGA 350  
Db 16 TTCTGTGA 9

RESULT 166  
AW248747  
LOCUS  
DEFINITION  
 AW248747.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821119 3',  
 mRNA sequence.  
ACCESSION  
 AW248747  
VERSION  
 AW248747.1 GI:6591740  
KEYWORDS  
 EST.  
SOURCE  
 Homo sapiens (human)  
ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image.html](http://www.bio.llnl.gov/bbrp/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM5 row: L column: 1  
High quality sequence stop: 19.  
Location/Qualifiers

#### FEATURES

source

1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821008"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/notes="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 AACCCCA 308  
|||||||  
Db 16 AACCCCA 9

#### RESULT 168

AW249918/c  
LOCUS 2821753.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821753 3',  
DEFINITION mRNA sequence.

ACCESSION AW249918  
VERSION AW249918.1 GI:6592911  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2821753.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: K column: 2  
High quality sequence stop: 11.  
Location/Qualifiers

#### FEATURES

source

1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821753"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/notes="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 557 TTGATGAC 564  
|||||||  
Db 18 TTGATGAC 11

#### RESULT 169

CNS08V6Z

LOCUS 19 bp mRNA linear HTC 07-JAN-2003  
DEFINITION Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone FK0AAA44CD05 of strain 6-9 of Anopheles gambiae (African malaria mosquito).

ACCESSION BX029847  
VERSION BX029847.1 GI:27603128

KEYWORDS HTC.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

1 (bases 1 to 19)

#### REFERENCE

AUTHORS

TITLE Direct Submission

JOURNAL

Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [sequef@genoscope.cns.fr](mailto:sequef@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

#### FEATURES

source

1..19  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="6-9"  
/db\_xref="taxon:7165"  
/clone="FK0AAA44CD05"  
/plasmid="pME18S-FL"  
/note="end : 3-PRIME"

#### ORIGIN

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Query Match      1.3%; Score 8; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      178 CTCCTCTCT 185
      |||||
Db      4 CTCCTCTCT 11

RESULT 170
BM396331
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-2-E02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396331
VERSION     BM396331.1 GI:18196384
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 CTACCGCG 232
      |||||
Db      7 CTACCGCG 14

RESULT 172
BM397831
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-37-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397831
VERSION     BM397831.1 GI:18197884
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      326 TCACCGCG 333
      |||||
Db      7 TCACCGCG 14

RESULT 171
BM396766
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-25-A05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396766
VERSION     BM396766.1 GI:18196819
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)

```

```

COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 CTACCGCG 232
      |||||
Db      7 CTACCGCG 14

RESULT 172
BM397831
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-37-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397831
VERSION     BM397831.1 GI:18197884
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      360 GGCTGAGC 367
      |||||
Db      1 GGCTGAGC 8

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RESULT 173
BM398493
LOCUS
DEFINITION 5009-0-46-A02.t.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398493
VERSION
KEYWORDS
SOURCE
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 TCACCGCG 333
    |||||
Db 7 TCACCGCG 14

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 TCACCGCG 333
    |||||
Db 7 TCACCGCG 14

RESULT 174
BM400016
LOCUS
DEFINITION 5009-0-64-G07.t.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400016
VERSION
KEYWORDS
SOURCE
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

```

```

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368
    |||||
Db 3 GCTGAGCC 10

RESULT 175
BM401275
LOCUS
DEFINITION 5009-0-85-B03.t.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM401275
VERSION
KEYWORDS
SOURCE
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368
    |||||
Db 2 GCTGAGCC 9

RESULT 176
BQ583648
LOCUS
DEFINITION E011977-024-005-G09-SP6 MP1Z-ADIS-024-Inflorance Beta vulgaris
cDNA clone 024-005-G09 5-PRIME, mRNA sequence.
ACCESSION BQ583648

```

```

VERSION BQ583648.1 GI:26113225
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 5 row: G column: 09
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
1. .19
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:183047"
/db_xref="taxon:161934"
/clone="024-005-G09"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/clone_lib="MPZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GACTGGGA 206
|||||
Db 2 GACTGGGA 9

RESULT 177
BQ587387
LOCUS S014305-024-010-H05-SP6 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-010-H05 5-PRIME, mRNA sequence.
ACCESSION BQ587387
VERSION BQ587387.1 GI:26116969
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPZ

```

```

TITLE
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT 12472698
Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 10 row: H column: 05
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
1. .19
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185481"
/db_xref="taxon:161934"
/clone="024-010-H05"
/tissue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MPZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CTGCGCGC 222
|||||
Db 8 CTGCGCGC 15

RESULT 178
BQ594129/c
LOCUS BQ594129
DEFINITION BQ594129 19 bp mRNA linear EST 06-DEC-2002
ACCESSION BQ594129
VERSION BQ594129.1 GI:26123712
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPZ

```

Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaa@piz-koeln.mpg.de  
 Insert Length: 19 Std Error: 0.00  
 Plate: 25 row, B column: 01  
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

# FEATURES

source  
 1. .19  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:192727"  
 /db\_xref="taxon:161934"  
 /clone="024-025-B01"  
 /issue\_type="developing root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MPZ-ADIS-024-developing root"  
 /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
 SP6-Sali-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TTCAGTTC 511  
 |||||  
 Db 12 TTCAGTTC 5

## RESULT 179

EX548528/c  
 LOCUS  
 DEFINITION  
 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse101e02\_q1c, mRNA sequence.

ACCESSION  
 EX548528  
 VERSION  
 EX548528.1 GI:33298765  
 KEYWORDS  
 EST.

## SOURCE

ORGANISM  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

## REFERENCE

AUTHORS  
 Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE  
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL  
 Genome Biol. 4 (10), R63 (2003)

## MEDLINE

22881942

## PUBMED

14519198

## COMMENT

Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from

the 3' end.

# FEATURES

source  
 1. .19  
 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse101e02\_q1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

## ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 AGCCCTG 260  
 |||||  
 Db 17 AGCCCTG 10

## RESULT 180

CO1216  
 LOCUS  
 DEFINITION  
 HUMG30007928 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.

## ACCESSION

CO1216  
 VERSION  
 CO1216.1 GI:1433446

## KEYWORDS

EST.

## SOURCE

ORGANISM  
 Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS  
 Okubo, K.

TITLE  
 BodyMap: human gene expression database

JOURNAL  
 Unpublished (1995)

COMMENT  
 Contact: Okubo, K.

Institute for Molecular and Cellular Biol

Osaka University

1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111 (ex.3315)

Email: kousaku@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DDBJ

since 1993. For the abundance information of clones with this

sequence in this library and as well as in other 3'-directed

libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap'. The

sequences of the clones represented by this GS sequences is also

found there.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="adult"

/clone\_lib="Human adult (K.Okubo)"

/note="One or more human adult tissue"

## ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.9e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCTGTG 349

|||||

Db 12 CTTCTGTG 19

## RESULT 181

CO1993/c



```

LOCUS       C01993              19 bp    mRNA    linear    EST 31-DEC-2002
DEFINITION  HUMGS004016 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCESSION   C01993
VERSION     C01993.1  GI:1434223
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Okubo,K.
TITLE       BodyMap; human gene expression database
JOURNAL     Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kouaoku@imcb.osaka-u.ac.jp
            We are not submitting the same cDNA sequence redundantly to DBJ
            since 1993. For the abundance information of clones with this
            sequence in this library and as well as in other 3'-directed
            libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
            sequences of the clones represented by this GS sequences is also
            found there.

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"

ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      210 AGACCCCTG 217
        |||||
Db       19 AGACCCCTG 12

RESULT 182
C21102/c

LOCUS       C21102              19 bp    mRNA    linear    EST 31-DEC-2002
DEFINITION  HUMGS002625 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
sequence.
ACCESSION   C21102
VERSION     C21102.1  GI:1622212
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Okubo,K.
TITLE       BodyMap; human gene expression database
JOURNAL     Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kouaoku@imcb.osaka-u.ac.jp
            We are not submitting the same cDNA sequence redundantly to DBJ
            since 1993. For the abundance information of clones with this
            sequence in this library and as well as in other 3'-directed
            libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
            sequences of the clones represented by this GS sequences is also
            found there.

LOCUS       C21102              19 bp    mRNA    linear    EST 31-DEC-2002
DEFINITION  HUMGS0002625 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCESSION   C21102
VERSION     C21102.1  GI:1622212
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
TITLE       Gene discovery and microarray analysis of cacao (Theobroma cacao
JOURNAL     Planta 216 (2), 255-264 (2002)
MEDLINE     22337596
PUBMED      12447539
COMMENT     Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644
            Email: Paul.Jones@eu.affem.com
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Theobroma cacao"
                     /mol_type="mRNA"
                     /strain="Amelonado type"
                     /db_xref="taxon:3641"
                     /clone="Cac BL 1268"
                     /tissue_type="Mature leaf and mature bean"
                     /cell_type="Whole organ"
                     /dev_stage="maturity"
                     /lab_host="XL-1 Blue MRF"
                     /clone_lib="Cac BL (Bean and Leaf from Amelonado type
                     Cacao)"
                     /note="vector: pBK-CMV; Bean and leaf tissue from an
                     Amelonado type Cacao tree."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 CCCCAACC 310
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Db       16 CCCCAACC 9

```

```

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"

ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      317 TGAGGATC 324
        |||||
Db       8 TGAGGATC 1

RESULT 183
CA794263/c

LOCUS       CA794263              19 bp    mRNA    linear    EST 05-DEC-2002
DEFINITION  Theobroma cacao cDNA clone Cac_BL_1268 5', mRNA sequence.
ACCESSION   CA794263
VERSION     CA794263.1  GI:26051339
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
TITLE       Gene discovery and microarray analysis of cacao (Theobroma cacao
JOURNAL     Planta 216 (2), 255-264 (2002)
MEDLINE     22337596
PUBMED      12447539
COMMENT     Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644
            Email: Paul.Jones@eu.affem.com
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Theobroma cacao"
                     /mol_type="mRNA"
                     /strain="Amelonado type"
                     /db_xref="taxon:3641"
                     /clone="Cac BL 1268"
                     /tissue_type="Mature leaf and mature bean"
                     /cell_type="Whole organ"
                     /dev_stage="maturity"
                     /lab_host="XL-1 Blue MRF"
                     /clone_lib="Cac BL (Bean and Leaf from Amelonado type
                     Cacao)"
                     /note="vector: pBK-CMV; Bean and leaf tissue from an
                     Amelonado type Cacao tree."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 CCCCAACC 310
        |||||
Db       16 CCCCAACC 9

```

```

RESULT 184
CA967211/C
LOCUS
DEFINITION
  19 bp mRNA linear EST 03-JAN-2003
  Cc1l01a03k1lf2 Carp liver library 1 Cyprinus carpio cDNA clone
  03k11 5', mRNA sequence.
ACCESSION
  CA967211
KEYWORDS
  CA967211.1 GI:27493768
SOURCE
  EST.
ORGANISM
  Cyprinus carpio (common carp)
  Cyprinus carpio
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE
  1 (bases 1 to 19)
  Gracey,A.Y., Fraser,B., Li,W. and Cossins,A.R.
  Microarray and EST analysis of the carp (Cyprinus carpio)
  transcriptome during environmental stress
  Unpublished (2003)
JOURNAL
  Contact: Andrew R. Cossins
  Laboratory for Environmental Gene Regulation
  University of Liverpool
  School of Biological Sciences, The Biosciences Building, Crown
  Street, Liverpool, United Kingdom, L69 7ZB
  Tel: +44(0)151-795-4510
  Fax: +44(0)151-795-4431
  Email: cossins@liv.ac.uk
  Vector has been trimmed from this EST.
  Plate: 03 row: k column: 11
  Seq primer: Triplex 5' LD (5'-CTCGGAAGCGCGCATTTGTTGGT-3')
  High quality sequence start: 9
  High quality sequence stop: 17.
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    /sex="Male & female"
    /tissue_type="Liver"
    /dev_stage="Adult"
    /lab_host="E.coli Electromax DH10B"
    /clone_lib="Carp liver library 1"
    /notes="Vector: pTriplex2; Site1: sfll GGCATTACGGCC;
    Site2: sfll GCGCGCTCGGC; Normalized cDNA library
    prepared from liver of warm, cold and hypoxia challenged
    animals"
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    /mol_type="mRNA"
    /db_xref="taxon:7962"
    /clone="03k11"
    /sex="Male & female"
    /tissue_type="Liver"
    /dev_stage="Adult"
    /lab_host="E.coli Electromax DH10B"
    /clone_lib="Carp liver library 1"
    /notes="Vector: pTriplex2; Site1: sfll GGCATTACGGCC;
    Site2: sfll GCGCGCTCGGC; Normalized cDNA library
    prepared from liver of warm, cold and hypoxia challenged
    animals"
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  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 280 GTGGCCGA 287
  Db 18 GTGGCCGA 11

RESULT 185
CF294232
LOCUS
DEFINITION
  30DGS--03-L01.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
  sativa cDNA clone 30DGS--03-L01, mRNA sequence.
ACCESSION
  CF294232
KEYWORDS
  CF294232.1 GI:33663265
SOURCE
  EST.
ORGANISM
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..19
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="7LEAF--02-J10"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library I (7LEAF)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
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    RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 259 TGCTACGA 266
  Db 2 TGCTACGA 9

RESULT 186
CF298891
LOCUS
DEFINITION
  19 bp mRNA linear EST 15-AUG-2003
  7LEAF--02-J10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa cDNA clone 7LEAF--02-J10, mRNA sequence.
ACCESSION
  CF298891
KEYWORDS
  CF298891.1 GI:33670652
SOURCE
  EST.
ORGANISM
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
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  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 259 TGCTACGA 266
  Db 2 TGCTACGA 9

TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
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    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="30DGS--03-L01"
    /tissue_type="leaf"
    /dev_stage="30 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
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    1..19
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
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    RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 259 TGCTACGA 266
  Db 2 TGCTACGA 9

TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
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    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="30DGS--03-L01"
    /tissue_type="leaf"
    /dev_stage="30 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
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    /tissue_type="leaf"
    /dev_stage="30 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
    /notes="Vector: PCR4-TOPO; Site1: SCORI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 259 TGCTACGA 266
  Db 2 TGCTACGA 9

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## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGAGGG 492  
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 Db 3 GGGAGGG 10

## RESULT 187

CF303019 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF1--01-B20.g1 ABF3-overexpressing transgenic rice lambda phage  
 DEFINITION cDNA library (ABF1) Oryza sativa cDNA clone ABF1--01-B20, mRNA  
 sequence.

ACCESSION CF303019.1 GI:33674780  
 VERSION  
 KEYWORDS EST.

## SOURCE

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="ABF1--01-B20"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="ABF3-overexpressing transgenic rice lambda  
 phage cDNA library (ABF1)"  
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Leaf was dried for 2hrs. cDNA was inserted into\_  
 lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
 with XhoI site. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497  
 |||||  
 Db 12 GGGCTGCA 19

## RESULT 188

CF305417 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS CLD1--01-K13.bl Rice cold treated leaf plasmid cDNA library (CLD1)  
 DEFINITION Oryza sativa cDNA clone CLD1--01-K13, mRNA sequence.

ACCESSION CF305417  
 VERSION

## KEYWORDS

SOURCE EST.  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source  
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 (CLD1)"  
 /notes="Vector: PCR4-TOPO; Site1: EcoRI; Leaf was  
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 mRNA was reverse transcribed and then used for PCR."

## ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTAGAAAA 461  
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 Db 12 GTAGAAAA 19

## RESULT 189

CF306280/c 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS HDAL--03-E08.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
 DEFINITION cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-E08, mRNA  
 sequence.

ACCESSION CF306280  
 VERSION CF306280.1 GI:33678041  
 KEYWORDS EST.

## SOURCE

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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 Location/Qualifiers  
 /organism="Oryza sativa"

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/mol_type="mRNA"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
  phage CDNA library I (HDAL)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
  XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
  was inserted into lambda Uni-ZAP XR vector at 5' end with
  EcoRI and 3' end with XhoI site. mRNA was derived from
  rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CCGCTGGG 61
|||||
Db 12 CCGCTGGG 5

RESULT 190
LOCUS CF306449
DEFINITION HDAL--03-002.g1 OSHDA1-overexpressing transgenic rice lambda phage
  cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-002, mRNA
  sequence.
ACCESSION CF306449
VERSION CF306449.1 GI:33678210
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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      /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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        reverse transcribed and then used for PCR. mRNA was
        derived from rice Histone Deacetylase overexpression
        line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
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Db 1 GCTACGTA 8

RESULT 192
LOCUS CF319596/c
DEFINITION HD--10-C14.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION CF319596
VERSION CF319596.1 GI:33691357
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)

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Qy 490 GGCCTGCA 497
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Db 11 GGCCTGCA 18

RESULT 191
LOCUS CF316935
DEFINITION HD--06-H01.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--06-H01, mRNA sequence.
ACCESSION CF316935
VERSION CF316935.1 GI:33688696
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
  source
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      /organism="Oryza sativa"
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        reverse transcribed and then used for PCR. mRNA was
        derived from rice Histone Deacetylase overexpression
        line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
|||||
Db 1 GCTACGTA 8

RESULT 192
LOCUS CF319596/c
DEFINITION HD--10-C14.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION CF319596
VERSION CF319596.1 GI:33691357
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)

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AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
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                cDNA library (HD)"
                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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                derived from rice Histone Deacetylase overexpression
                line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 TTCAAAAA 50
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        18 TTCAAAA 11

RESULT 193
CF326845
LOCUS      CF326845      19 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION  CF326845
VERSION     CF326845.1 GI:33801944
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 19)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1. .19
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="HD--10-C14"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDACL-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 TTCAAAAA 50
        |||||
        18 TTCAAAA 11

RESULT 193
CF326845
LOCUS      CF326845      19 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION  CF326845
VERSION     CF326845.1 GI:33801944
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 19)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1. .19
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="HD--10-C14"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"

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              /lab_host="E.coli DH10B"
              /clone_lib="Rice callus plasmid cDNA library (NACL)"
              /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
              with oligoribonucleotides and then used as templates for
              RT-PCR."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      454 GTAGAAAA 461
        |||||
        11 GTAGAAAA 8

RESULT 194
CF337272
LOCUS      CF337272      19 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--07-K10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-K10, mRNA sequence.
ACCESSION  CF337272
VERSION     CF337272.1 GI:33822933
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 19)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1. .19
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="JMT--07-K10"
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                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                cDNA library (JMT)"
                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                was reverse transcribed and then used for PCR. mRNA was
                prepared from Arabidopsis Jasmonate Carboxyl
                methyltransferase overexpression line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      454 GTAGAAAA 461
        |||||
        11 GTAGAAAA 18

RESULT 195
CF340173
LOCUS      CF340173      19 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION RCL1--07-C20.g1 Regenerated callus lambda phage cDNA library (RCL1)
            Oryza sativa cDNA clone RCL1--07-C20, mRNA sequence.

```

```

ACCESSION   CF340173
VERSION     CF340173.1
KEYWORDS    GI:33828707
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE   1 (bases 1 to 19)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     1..19
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="RCL1--07-C20"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E. coli SOLa"
     /clone_lib="Regenerated callus lambda phage cDNA library
     (RCL1)"
     /notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
     end with SstI and 3' end with XhoI site. Callus was
     induced on 2N6 media for 30 days and cultured for 36hrs on
     regenerated media"

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  96 AGTGAAGA 103
    |||||
Db   8 AGTGAAGA 15

RESULT 196
CF929669
LOCUS      CF-01-R-E08 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
DEFINITION CF-01-R-E08(5'), mRNA sequence.
ACCESSION   CF929669
VERSION     CF929669.1
KEYWORDS    GI:38278141
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 19)
            /lab_host="E. coli SOLa"
            /clone="RCL1--07-C20"
            /tissue_type="adipose tissue"
            /dev_stage="24 months old"
            /lab_host="XLI-BlueMRP" strain"
            /clone_lib="Bos taurus CF-24-HW cDNA library"
            /note="Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I"

REFERENCE   1 (bases 1 to 19)
AUTHORS    Yoon,D.H., Lee,S.H., Lee,J.H., Sang,B.C. and Oh,S.J.
TITLE      Gene Expression Profiling of the Bovine adipose tissues
JOURNAL    Unpublished (2003)
COMMENT    Contact: Dr. Du-Hak Yoon
            National Livestock Research Institute, RDA
            564 Omoekchun-dong, Suwon, 441-350, Korea
            Tel: 82 31 290 1593
            Fax: 82 31 290 1792
            Email: dhyoon@rda.go.kr
            Insert Length: 19 Std Error: 0.00
            Seq primer: ATTAACCCCTCACTAAG

FEATURES             Location/Qualifiers
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     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUC1M0029N17"
     /sex="Male"
     /lab_host="E. Coli strain XLI0-Gold, TI-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUC1M library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
     musculus C57BL/6J (male) was obtained from the Jackson
     Laboratory Mouse DNA Resource
     (http://www.jax.org/resources/documents/dnares/). The DNA
     was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 CCTGGGCC 220  
|||||||  
Db 9 CCTGGGCC 2

## RESULT 198

AZ315768  
LOCUS AZ315768 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0033F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0033F01 F, genomic survey sequence.

ACCESSION AZ315768  
VERSION AZ315768.1 GI:10362759  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: F column: 01

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

source

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TTTCCTTTA 38  
|||||||  
Db 12 TTTCCTTTA 19

## RESULT 199

AZ318731  
LOCUS AZ318731 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0038G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0038G08 F, genomic survey sequence.

ACCESSION AZ318731  
VERSION AZ318731.1 GI:10368989  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: G column: 08

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

source

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0038G08"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CTACGTAG 97  
|||||||  
Db 3 CTACGTAG 10

## RESULT 200

AZ318731/c  
LOCUS 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0038G08F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0038G08 F, genomic survey sequence.

ACCESSION AZ318731  
VERSION AZ318731.1 GI:10368989  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

## JOURNAL

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: G column: 08

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UGCLM0038G08"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CTACGTAG 97  
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Db 10 CTACGTAG 3

## RESULT 201

## AZ327390

## LOCUS

19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0050L09R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0050L09 R, genomic survey sequence.

ACCESSION AZ327390  
VERSION AZ327390.1 GI:10386092  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

## JOURNAL

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0050 row: L column: 09

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UGCLM0050L09"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 TCCTTTTG 543  
|||||||  
Db 1 TCCTTTTG 8

RESULT 202  
AZ328922/c

LOCUS AZ328922 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0052L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0052L22 R, genomic survey sequence.

ACCESSION AZ328922  
VERSION AZ328922.1 GI:10389127  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0052 row: 1 column: 22

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0052L22"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTAGAAAA 461  
|||||||  
Db 9 GTAGAAAA 2

RESULT 203  
AZ329293/c

LOCUS AZ329293 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0053A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0053A03 R, genomic survey sequence.

ACCESSION AZ329293  
VERSION AZ329293.1 GI:10389864  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0053 row: A column: 03

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0053A03"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAAGCTTT 476

|||||  
Db 9 AGAAGCTTT 2

## RESULT 204

AZ345500 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0080G01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G01 F, genomic survey sequence.

ACCESSION AZ345500

VERSION AZ345500.1 GI:10424737

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: G column: 01

Seq primer: CGTGTGAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTTTTA 437

|||||  
Db 8 TATTTTTA 15

## RESULT 205

AZ345954 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0080C03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080C03 R, genomic survey sequence.

ACCESSION AZ345954

VERSION AZ345954.1 GI:10425191

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: O column: 23

Seq primer: CACACAGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080C03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 GTAGTGAA 101  
|||||||  
Db 13 GTAGTGAA 6

## RESULT 206

AZ346697

LOCUS

DEFINITION AZ346697 19 bp DNA linear GSS 29-SEP-2000  
clone UNGC1M0082J06 F, genomic survey sequence.

ACCESSION

AZ346697

VERSION

AZ346697.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0082 row: J column: 06

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0082J06"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439  
|||||||  
Db 2 TTTTACT 9

## RESULT 207

AZ358656/c

LOCUS

DEFINITION AZ358656 19 bp DNA linear GSS 02-OCT-2000  
clone UUGC1M0101K12 F, genomic survey sequence.

ACCESSION

AZ358656

VERSION

AZ358656.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0101 row: K column: 12

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0101K12"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TGTGAGGA 353  
 |||||  
 Db 19 TGTGAGGA 12

## RESULT 208

AZ363907  
 LOCUS AZ363907 19 bp DNA linear GSS 02-OCT-2000  
 DEFINITION IM0109113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0109113 R, genomic survey sequence.

ACCESSION AZ363907  
 VERSION AZ363907.1 GI:10477607  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 1 (bases 1 to 19)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0109 row: I column: 13  
 Seq primer: CACACGGAACACGATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0109113"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436  
 |||||  
 Db 8 TTATTTT 15

## RESULT 209

AZ370656/c  
 LOCUS AZ370656 19 bp DNA linear GSS 02-OCT-2000  
 DEFINITION IM0121F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0121F18 R, genomic survey sequence.

ACCESSION AZ370656  
 VERSION AZ370656.1 GI:10484356  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 1 (bases 1 to 19)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0121 row: F column: 18  
 Seq primer: CACACGGAACACGATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0121F18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TGGAAATAC 449

Db 13 TGGAAATAC 6

## RESULT 210

AZ375581

LOCUS

DEFINITION IM0129E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129E05 F, genomic survey sequence.

ACCESSION

AZ375581

VERSION

GSS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center

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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: E column: 05  
Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0129E05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 TTATCTTC 148

Db 9 TTATCTTC 16

## RESULT 211

AZ387157

LOCUS

DEFINITION IM0146E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0146E20 R, genomic survey sequence.

ACCESSION

AZ387157

VERSION

GSS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center

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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0146 row: E column: 20  
Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0146E20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 TTTCCTTA 38  
|||||||  
Db 9 TTTCCTTA 16

## RESULT 212

AZ392507  
LOCUS 19 bp DNA linear GSS 03-OCT-2000  
DEFINITION M0155H11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0155H11 F, genomic survey sequence.

ACCESSION AZ392507  
VERSION AZ392507.1 GI:10507579  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0155 row: H column: 11

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0155H11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note=Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 ACCTACCT 86  
|||||||  
Db 3 ACCTACCT 10

## RESULT 213

AZ393531  
LOCUS 19 bp DNA linear GSS 03-OCT-2000  
DEFINITION M0156F07R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0156F07 R, genomic survey sequence.

ACCESSION AZ393531  
VERSION AZ393531.1 GI:10508603  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: F column: 07

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0156F07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note=Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TTTCTTTA 38  
|||||||  
Db 17 TTTCTTTA 10

RESULT 214  
AZ410317/c  
LOCUS  
DEFINITION  
1M0182L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0182L02 R, genomic survey sequence.

ACCESSION  
AZ410317  
VERSION  
AZ410317.1 GI:10534330  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0182 row: L column: 02  
Seg primer: CACACAGAAACGCTATGACC  
Class: plasmid ends

High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0182L02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 AAGCCTGG 486  
|||||||  
Db 9 AAGCCTGG 2

RESULT 215  
AZ412553/c

LOCUS  
DEFINITION  
1M0186M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0186M03 F, genomic survey sequence.

ACCESSION  
AZ412553  
VERSION  
AZ412553.1 GI:10536566  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0186 row: M column: 03  
Seg primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0186M03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 CCCACACC 310  
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Db 14 CCCACACC 7

## RESULT 216

AZ414372 19 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION  
IM0188G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0188G18 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0188 row: G column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

## source

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0188G18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTTTACC 40  
|||||||  
Db 7 TCTTTACC 14

## RESULT 217

AZ424415 19 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION  
IM0204G02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0204G02 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0204 row: G column: 02  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

## source

1..19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0204G02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATA 448  
|||||||  
Db 5 CTGGAATA 12

RESULT 218  
AZ424415/c  
LOCUS  
DEFINITION 1M0204G02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0204G02 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ424415 19 bp DNA linear GSS 03-OCT-2000  
1M0204G02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0204G02 F, genomic survey sequence.  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
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plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0204 row: G column: 02  
Seq primer: CTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0204G02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 TCCAGACA 524  
|||||||  
Db 9 TCCAGACA 2

RESULT 219  
AZ429008/c  
LOCUS  
DEFINITION 1M0212E07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0212E07 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ429008 19 bp DNA linear GSS 03-OCT-2000  
1M0212E07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0212E07 R, genomic survey sequence.  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0212 row: E column: 07  
Seq primer: CACACAGGAACACGATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0212E07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATTCAAA 48  
 |||||  
 Db 16 AATTCAAA 9

RESULT 220  
 AZ436629  
 LOCUS 19 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0224019F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0224019 F, genomic survey sequence.

ACCESSION AZ436629  
 VERSION 1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0224 row: 0 column: 19

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19  
 Location/Qualifiers

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0224019"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTTGATGA 19  
 |||||  
 Db 12 CTTGATGA 19

## RESULT 221

AZ445457

LOCUS 19 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0241J13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0241J13 F, genomic survey sequence.

ACCESSION AZ445457  
 VERSION 1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0241 row: J column: 13

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19  
 Location/Qualifiers

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0241J13"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436  
|||||  
Db 10 TTATTTT 17

## RESULT 222

AZ447252/c

LOCUS

DEFINITION 1M0244M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0244M24 F, genomic survey sequence.

ACCESSION

AZ447252

VERSION

A2447252.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: M column: 24

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC1M0244M24"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 GGTGATG 562  
|||||  
Db 13 GGTGATG 6

## RESULT 223

AZ454430

LOCUS

DEFINITION 1M0256F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0256F21 F, genomic survey sequence.

ACCESSION

AZ454430

VERSION

AZ454430.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0256 row: F column: 21

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC1M0256F21"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GACTGGGA 206  
|||||||  
DB 5 GACTGGGA 12

## RESULT 224

AZ475705/c  
LOCUS AZ475705 19 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0294B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0294B02 F, genomic survey sequence.

ACCESSION AZ475705  
VERSION AZ475705.1 GI:10633830  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0294 row: B column: 02

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0294B02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AGCCTGGG 487  
|||||||  
DB 18 AGCCTGGG 11

## RESULT 225

AZ484016/c  
LOCUS AZ484016 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0310J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0310J10 F, genomic survey sequence.

ACCESSION AZ484016  
VERSION AZ484016.1 GI:10648549  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0310 row: J column: 10

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0310J10"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 TTGGTTAT 144  
|||||||  
Db 8 TTGGTTAT 1

## RESULT 226

AZ484528  
LOCUS 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0311J03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0311J03 F, genomic survey sequence.

ACCESSION AZ484528  
VERSION AZ484528.1 GI:10649472  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0311 row: J column: 03  
Seq primer: CGTTGTAACGACGGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0311J03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGGGCTAA 65  
|||||||  
Db 3 TGGGCTAA 10

## RESULT 227

AZ485264/c  
LOCUS 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0312002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0312002 R, genomic survey sequence.

ACCESSION AZ485264  
VERSION AZ485264.1 GI:10650911  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0312 row: O column: 02  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0312002"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 CACCTCCT 250  
|||||||  
Db 8 CACCTCCT 1

RESULT 228  
AZ493833/c  
LOCUS  
DEFINITION  
AZ493833  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ493833 19 bp DNA linear GSS 05-OCT-2000  
1M0328P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0328P11 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ493833 1 GI:10667884  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0328 row: P column: 11  
Seq primer: CACACAGGAACACGCTATGACC  
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High quality sequence stop: 19.  
Location/Qualifiers  
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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0328P11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PWD42nv; Purified genomic DNA from M.  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 CCCCAACC 310  
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Db 15 CCCCAACC 8

RESULT 229  
AZ495849/c  
LOCUS  
DEFINITION  
AZ495849  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ495849 19 bp DNA linear GSS 05-OCT-2000  
1M0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0331N22 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ495849 1 GI:10671571  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 480 AGCCTGGG 487  
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Db 8 AGCCTGGG 1

RESULT 230  
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LOCUS  
DEFINITION  
1M0349D11f Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0349D11 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ507472 19 bp DNA linear GSS 05-OCT-2000  
1M0349D11f Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0349D11 F, genomic survey sequence.  
AZ507472.1 GI:10688788  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Islam, H., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

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Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0349 row: D column: 11  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: Plasmid ends  
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source

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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 CAAGGCTG 364  
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Db 12 CAAGGCTG 5

RESULT 231  
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LOCUS  
DEFINITION  
1M0361H02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0361H02 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ514386 19 bp DNA linear GSS 05-OCT-2000  
1M0361H02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0361H02 F, genomic survey sequence.  
AZ514386.1 GI:10695702  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

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plasmid inserts  
Unpublished (2000)

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University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: H column: 02  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: Plasmid ends  
High quality sequence stop: 19.

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/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 ACAGTGCT 117  
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Db 1 ACAGTGCT 8

RESULT 232  
AZ514722/c

LOCUS AZ514722 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0361C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0361C10 R, genomic survey sequence.

ACCESSION AZ514722  
VERSION AZ514722.1 GI:10696038  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: C column: 10  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES  
source

1..19  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
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FEATURES  
source

1..19  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CAAAAATG 52  
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Db 18 CAAAAATG 11

RESULT 233  
AZ514774

LOCUS AZ514774 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0361N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0361N11 R, genomic survey sequence.

ACCESSION AZ514774  
VERSION AZ514774.1 GI:10696090  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: N column: 11  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361N11"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 338 TCTACTTC 345  
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 Db 6 TCTACTTC 13

RESULT 234  
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 clone UGCGIM0363M07 F, genomic survey sequence.

ACCESSION AZ579084  
 VERSION AZ579084.1 GI:11693545  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

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JOURNAL Unpublished (2000)

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 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0363 row: M column: 07

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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source

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 492 GCTGCATG 499  
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 Db 5 GCTGCATG 12

RESULT 235  
 AZ581123

LOCUS 1M0363N08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCG1M0363N08 R, genomic survey sequence.

ACCESSION AZ581123

VERSION AZ581123.1 GI:11695820

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

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Unpublished (2000)

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 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0369 row: N column: 08

Seq primer: CACACAGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGIM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 114 TGCTACAT 121  
|||||||  
Db 12 TGCTACAT 19

RESULT 236  
AZ585820  
LOCUS  
DEFINITION  
IM0391115F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0391115 F, genomic survey sequence.

ACCESSION  
AZ585820  
VERSION  
AZ585820.1 GI:11708010  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0391 row: I column: 15  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0391115"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 360 GGCTGAGC 367  
|||||||  
Db 10 GGCTGAGC 17

RESULT 237  
AZ586377/c  
LOCUS  
DEFINITION  
IM0392A15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGCIM0392A15 F, genomic survey sequence.

ACCESSION  
AZ586377  
VERSION  
AZ586377.1 GI:11708567  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0392 row: A column: 15  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0392A15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TGCAATA 408  
|||||  
Db 15 TGCAATA 8

## RESULT 238

AZ588155  
LOCUS  
DEFINITION 1M0396110F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0396110 F, genomic survey sequence.

ACCESSION AZ588155  
VERSION 1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0396 row: I column: 10

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC1M0396110"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AAAAATGT 53  
|||||  
Db 3 AAAAATGT 10

## RESULT 239

AZ591963  
LOCUS  
DEFINITION 1M0402P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0402P23 F, genomic survey sequence.

ACCESSION AZ591963  
VERSION 1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0402 row: P column: 23

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC1M0402P23"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 ATTGCTCT 181  
|||||  
Db 8 ATTGCTCT 15

## RESULT 240

AZ610451  
LOCUS  
DEFINITION  
M0435C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0435C18 R, genomic survey sequence.

ACCESSION  
AZ610451

VERSION  
AZ610451.1 GI:11732641

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 19)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0435 row: C column: 18

Seq primer: CACACAGGACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0435C18"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGGCTG 387  
|||||  
Db 7 GCGGCTG 14

## RESULT 241

AZ611716  
LOCUS  
DEFINITION  
M0439B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0439B15 F, genomic survey sequence.

ACCESSION  
AZ611716

VERSION  
AZ611716.1 GI:11733906

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0438 row: B column: 15

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0439B15"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 CGCGCGCC 337  
|||||  
Db 11 CGCGCGCC 4

## RESULT 242

AZ623283  
LOCUS  
DEFINITION 1M0460N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0460N18 R, genomic survey sequence.

ACCESSION AZ623283  
VERSION AZ623283.1 GI:11745473  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: N column: 18

Seq primer: CACACAGGAACGATGTACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

## FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 CACCTGGT 241  
|||||  
Db 2 CACCTGGT 9

## RESULT 243

AZ626685/c

## LOCUS

DEFINITION 1M0467M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0467M01 F, genomic survey sequence.

ACCESSION AZ626685  
VERSION AZ626685.1 GI:11748875  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0467 row: M column: 01

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0467M01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 GAAGGGCT 494  
|||||||  
Db 19 GAAGGGCT 12

RESULT 244  
AZ654747  
LOCUS  
DEFINITION  
1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0529F08 F, genomic survey sequence.

ACCESSION  
AZ654747  
VERSION  
AZ654747.1 GI:11791893  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: F column: 08  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

1..19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0529F08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436  
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Db 4 TTATTTT 11

RESULT 245  
AZ655467  
LOCUS  
DEFINITION  
1M0530O17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0530O17 F, genomic survey sequence.

ACCESSION  
AZ655467  
VERSION  
AZ655467.1 GI:11792529  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0530 row: O column: 17  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

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Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0530O17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 GGCTGAGC 367  
|||||  
Db 10 GGCTGAGC 17

RESULT 246  
AZ655467/c  
LOCUS  
DEFINITION 1M0530017F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0530017 F, genomic survey sequence.

ACCESSION AZ655467  
VERSION AZ655467.1 GI:11792529  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0530 row: 0 column: 17

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

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Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0530017"  
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 AGGCATCA 415  
|||||  
Db 13 AGGCATCA 6

RESULT 247  
AZ655870/c

## LOCUS

DEFINITION 1M0531N06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0531N06 F, genomic survey sequence.

ACCESSION AZ655870  
VERSION AZ655870.1 GI:11793016  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0531 row: N column: 06

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

1. .19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0531N06"  
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G1|4732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 AGTCTGAG 320  
|||||||  
Db 17 AGTCTGAG 10

RESULT 248  
AZ658087/c

LOCUS  
DEFINITION 1M0534J09R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0534J09 R, genomic survey sequence.

ACCESSION AZ658087  
VERSION AZ658087.1 GI:11795233  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: J column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

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Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UGCM0534J09"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G1|4732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 TCTGTGAG 351  
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Db 13 TCTGTGAG 6

RESULT 249  
AZ664265/c

LOCUS  
DEFINITION 1M0544A19F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0544A19 F, genomic survey sequence.

ACCESSION AZ664265  
VERSION AZ664265.1 GI:11801411  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0544 row: A column: 19

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1..19

Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UGCM0544A19"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGC 178  
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Db 8 GGAATTGC 1

## RESULT 250

AZ759944

LOCUS

DEFINITION 1M0553010F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0553010 F, genomic survey sequence.

ACCESSION AZ759944

VERSION AZ759944.1

KEYWORDS GI:12867253

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: 0 column: 10

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0553010"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30  
|||||||  
Db 4 GGAGGAAG 11

## RESULT 251

AZ759944/c

LOCUS

DEFINITION 1M0553010F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0553010 F, genomic survey sequence.

ACCESSION AZ759944

VERSION AZ759944.1

KEYWORDS GI:12867253

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: 0 column: 10

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0553010"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCTCTCC 187  
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 Db 11 CTTCTCTCC 4

RESULT 252  
 AZ764662/c  
 LOCUS  
 DEFINITION IM0561K11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0561K11 F, genomic survey sequence.

ACCESSION AZ764662.1 GI:12879855  
 VERSION AZ764662  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0561 row: K column: 11  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19

## FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0561K11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AGGGGCTG 378  
 |||||  
 Db 19 AGGGGCTG 12

RESULT 253  
 AZ769438

LOCUS  
 DEFINITION IM0570P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0570P09 F, genomic survey sequence.

ACCESSION AZ769438  
 VERSION AZ769438.1 GI:12889573  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0570 row: F column: 09  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19

## FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0570P09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ATTCAAAA 49  
|||||||  
Db 5 ATTCAAAA 12

## RESULT 254

AZ772446 19 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 1M0583016F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0583016 F, genomic survey sequence.

ACCESSION AZ772446  
VERSION AZ772446.1 GI:12895762  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0583 row: 0 column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0583016"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 TGACAGTG 115  
|||||||  
Db 9 TGACAGTG 16

## RESULT 255

AZ778302 19 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0013C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0013C02 F, genomic survey sequence.

ACCESSION AZ778302  
VERSION AZ778302.1 GI:12907800  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0013 row: 0 column: 02

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0013C02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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(http://www.jax.org/resources/documents/dnares/). The DNA

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 GTAGTGAA 101  
 |||||  
 Db 10 GTAGTGAA 3

RESULT 256  
 AZ778801/c  
 LOCUS  
 DEFINITION  
 2M0014013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0014013 F, genomic survey sequence.

ACCESSION  
 AZ778801  
 VERSION  
 AZ778801.1 GI:12908811  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0014 row: 0 column: 13  
 Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a

FEATURES  
source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0014013"  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 TTCAGTTC 511  
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 Db 17 TTCAGTTC 10

RESULT 257  
 AZ783702  
 LOCUS  
 DEFINITION  
 2M0025108R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0025108 R, genomic survey sequence.

ACCESSION  
 AZ783702  
 VERSION  
 AZ783702.1 GI:12918705  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0025 row: 1 column: 08  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0025108"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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FEATURES  
source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0025108"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 266 ACTGTGCC 273

Db 2 ACTGTGCC 9

## RESULT 258

AZ784693

LOCUS

DEFINITION AZ784693 19 bp DNA linear GSS 16-FEB-2001  
2M0027N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0027N18 R, genomic survey sequence.

ACCESSION

AZ784693

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0027 row: N column: 18

Seq primer: CACACAGGAACAGCTATGAC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

source

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/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0027N18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M.

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GTGCAAT 407

Db 12 GTGCAAT 19

## RESULT 259

AZ787588/c

LOCUS

DEFINITION AZ787588 19 bp DNA linear GSS 16-FEB-2001  
2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0034A07 F, genomic survey sequence.

ACCESSION

AZ787588

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D. Weiss,R.

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JOURNAL

COMMENT

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: A column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0034A07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M.

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GTGCAAT 407

Db 12 GTGCAAT 19

## RESULT 259

AZ787588/c

LOCUS

DEFINITION AZ787588 19 bp DNA linear GSS 16-FEB-2001  
2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0034A07 F, genomic survey sequence.

ACCESSION

AZ787588

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

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AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

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Niederhauser,A. and Wright,D. Weiss,R.

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: A column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

source

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0034A07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M.

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GTGCAAT 407

Db 12 GTGCAAT 19

## RESULT 259

AZ787588/c

LOCUS

DEFINITION AZ787588 19 bp DNA linear GSS 16-FEB-2001  
2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0034A07 F, genomic survey sequence.

ACCESSION

AZ787588

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

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AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D. Weiss,R.

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JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: A column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

source

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0034A07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M.

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GTGCAAT 407

Db 12 GTGCAAT 19

## RESULT 259

AZ787588/c

LOCUS

DEFINITION AZ787588 19 bp DNA linear GSS 16-FEB-2001  
2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0034A07 F, genomic survey sequence.

ACCESSION

AZ787588

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

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84112, USA

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 GTTCTTTT 37  
|||||||  
Db 8 GTTCTTTT 1

## RESULT 260

AZ789674

LOCUS

DEFINITION AZ789674 19 bp DNA linear GSS 16-FEB-2001  
2M0037L08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCG2M0037L08 R, genomic survey sequence.

ACCESSION

AZ789674

VERSION

AZ789674.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0037 row: L column: 08

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UGCG2M0037L08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

Laboratory Mouse DNA Resource

(http://www.fax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436  
|||||||  
Db 12 TTATTTT 19

## RESULT 261

AZ792828/c

LOCUS

DEFINITION AZ792828 19 bp DNA linear GSS 16-FEB-2001  
2M0045N01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCG2M0045N01 R, genomic survey sequence.

ACCESSION

AZ792828

VERSION

AZ792828.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: N column: 01

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

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/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UGCG2M0045N01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

Laboratory Mouse DNA Resource

(http://www.fax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGGCTGA 365  
|||||  
DB 11 AAGGCTGA 4

RESULT 262  
AZ794641  
LOCUS  
DEFINITION  
2M0048E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0048E05 R, genomic survey sequence.

ACCESSION  
AZ794641  
VERSION  
GI:12940815

KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0048 row: E column: 05  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0048E05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 CTGCTGGA 445  
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DB 10 CTGCTGGA 17

RESULT 263  
AZ795136/c  
LOCUS  
DEFINITION  
2M0049A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0049A16 F, genomic survey sequence.

ACCESSION  
AZ795136  
VERSION  
GI:12941845

KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0049 row: A column: 16  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0049A16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 TGCTACAT 121  
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 Db 14 TGCTACAT 7

RESULT 264  
 AZ798955/c  
 LOCUS  
 DEFINITION 2M0056K01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0056K01 F, genomic survey sequence.

ACCESSION AZ798955  
 VERSION AZ798955.1 GI:12949578  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0056 row: K column: 01  
 Seq primer: CGTTGTAACACGCGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0056K01"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AAGTTTCT 35  
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 Db 8 AAGTTTCT 1

RESULT 265  
 AZ800056  
 LOCUS  
 DEFINITION 2M0057E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0057E20 R, genomic survey sequence.

ACCESSION AZ800056  
 VERSION AZ800056.1 GI:12951797  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0057 row: E column: 20  
 Seq primer: CACACAGCAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0057E20"  
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 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 TGCTGGAA 446  
|||||  
Db 3 TGCTGGAA 10

RESULT 266  
AZ804026/c  
LOCUS  
DEFINITION  
2M0064007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0064007 R, genomic survey sequence.

ACCESSION  
AZ804026  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
1 (bases 1 to 19)  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0064 row: 0 column: 07  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

1. .19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0064007"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 TTCAGTTC 511  
|||||  
Db 17 TTCAGTTC 10

RESULT 267  
AZ805995

LOCUS  
DEFINITION  
2M0067F13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0067F13 R, genomic survey sequence.

ACCESSION  
AZ805995  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
1 (bases 1 to 19)  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
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JOURNAL  
Unpublished (2000)

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Contact: Robert B. Weiss  
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University of Utah  
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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0067 row: F column: 13  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

1. .19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0067F13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 TTTCTGGC 296  
|||||||  
Db 3 TTTCTGGC 10

## RESULT 268

AZ807749  
LOCUS 2M0070L17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0070L17 R, genomic survey sequence.

ACCESSION AZ807749  
VERSION 1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: L column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0070L17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 CCTGGAGC 255  
|||||||  
Db 12 CCTGGAGC 19

## RESULT 269

AZ810098  
LOCUS 2M0074N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0074N21 F, genomic survey sequence.

ACCESSION AZ810098  
VERSION 1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: N column: 21

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0074N21"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCTGCTA 263  
|||||||  
Db 12 CCCTGCTA 19

## RESULT 270

AZ811522 19 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0077M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0077M12 R, genomic survey sequence.

ACCESSION AZ811522  
VERSION AZ811522.1 GI:12979860  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0077 row: M column: 12

Seq primer: CACACGGAACGATGTAGC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

## FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGC 441  
|||||||  
Db 7 TTTACTGC 14

## RESULT 271

AZ813099 19 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0080P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0080P09 F, genomic survey sequence.

ACCESSION AZ813099  
VERSION AZ813099.1 GI:12983007  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: P column: 09

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

## FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0080P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 CGCAATAA 155  
|||||||  
Db 13 CGCAATAA 6

## RESULT 272

AZ815827/c 19 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0084K23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0084K23 F, genomic survey sequence.

ACCESSION AZ815827  
VERSION  
KEYWORDS  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0084 row: K column: 23  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

1..19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0084K23"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 ATGACCTT 422  
|||||||  
Db 17 ATGACCTT 10

## RESULT 273

AZ816318 19 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0085E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0085E05 F, genomic survey sequence.

ACCESSION AZ816318  
VERSION  
KEYWORDS  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0085 row: E column: 05  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

1..19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0085E05"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 AACGGCTG 164  
|||||||  
Db 6 AACGGCTG 13

## RESULT 274

AZ820818 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M00931118F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M00931118 F, genomic survey sequence.

ACCESSION AZ820818  
VERSION AZ820818.1 GI:12990726  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0093 row: 1 column: 18

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

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Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0093118"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGGC 219  
|||||||  
Db 10 ACCCTGGC 17

## RESULT 275

AZ822457 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0095D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0095D16 R, genomic survey sequence.

ACCESSION AZ822457  
VERSION AZ822457.1 GI:12992365  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0095 row: D column: 16

Seq primer: CACACAGGAACACGATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0095D16"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 TTCAGTTC 511  
 |||||  
 Db 9 TTCAGTTC 2

RESULT 276  
 AZ8271164/c  
 LOCUS  
 DEFINITION 2M0103M22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103M22 F, genomic survey sequence.

ACCESSION AZ8271164  
 VERSION AZ8271164.1 GI:12997072  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0103 row: M column: 22  
 Seq primer: CGTTGTAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
source

1. .19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0103M22"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 456 AGAAACC 463  
 |||||  
 Db 14 AGAAACC 7

RESULT 277  
 AZ830469  
 LOCUS  
 DEFINITION 2M0109C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0109C14 R, genomic survey sequence.

ACCESSION AZ830469  
 VERSION AZ830469.1 GI:13000377  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0109 row: C column: 14  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
source

1. .19  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
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 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 TGGGACCT 209  
|||||||  
Db 4 TGGGACCT 11

RESULT 278  
AZ834391  
LOCUS  
DEFINITION 2M0117N04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0117N04 F, genomic survey sequence.

ACCESSION AZ834391  
VERSION AZ834391.1 GI:13004299  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0117 row: N column: 04  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES  
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCATTACC 40  
|||||||  
Db 5 TCATTACC 12

RESULT 279  
AZ835621  
LOCUS  
DEFINITION 2M0129L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0129L21 R, genomic survey sequence.

ACCESSION AZ835621  
VERSION AZ835621.1 GI:13005529  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: L column: 21  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0129L21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES  
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TTCTGTGA 350  
|||||||  
Db 2 TTCTGTGA 9

## RESULT 280

AZ839642 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0135C23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0135C23 R, genomic survey sequence.

ACCESSION AZ839642  
VERSION AZ839642.1 GI:13009550  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0135 row: C column: 23  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 GGCGTGAG 78  
|||||||  
Db 5 GGCGTGAG 12

## RESULT 281

AZ841926 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0140K06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0140K06 F, genomic survey sequence.

ACCESSION AZ841926  
VERSION AZ841926.1 GI:13011750  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0140 row: K column: 06  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

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/organism="Mus musculus"  
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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGGCTGA 365  
|||||||  
Db 7 AAGGCTGA 14

RESULT 282  
AZ858730  
LOCUS  
DEFINITION  
2M0164104F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0164104 F, genomic survey sequence.

ACCESSION  
AZ858730  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0164 row: 1 column: 04  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 GCCGCTGC 225  
|||||||  
Db 5 GCCGCTGC 12

RESULT 283  
AZ858730/c  
LOCUS  
DEFINITION  
2M0164104F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0164104 F, genomic survey sequence.

ACCESSION  
AZ858730  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0164 row: 1 column: 04  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0164104"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 CAAGGCTG 364  
|||||  
Db 19 CAAGGCTG 12

## RESULT 284

AZ862758  
LOCUS 2M0170005R Mouse 10kb plasmid UUGCJM library Mus musculus genomic  
DEFINITION clone UUGC2M0170005 R, genomic survey sequence.

ACCESSION AZ862758  
VERSION AZ862758.1 GI:13060381  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0170 row: 0 column: 05

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19

/organism="Mus musculus"

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC2M0170005"

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGCJM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 ATTCAAAA 49  
|||||  
Db 12 ATTCAAAA 19

## RESULT 285

AZ862767  
LOCUS 2M0170A03R Mouse 10kb plasmid UUGCJM library Mus musculus genomic  
DEFINITION clone UUGC2M0170A09 R, genomic survey sequence.

ACCESSION AZ862767  
VERSION AZ862767.1 GI:13060399  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0170 row: A column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC2M0170A09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGCJM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 CACTGGAC 135  
 |||||  
 Db 10 CACTGGAC 17

## RESULT 286

AZ875430/c  
 LOCUS AZ875430 19 bp DNA linear GSS 21-FEB-2001  
 DEFINITION 2M0189K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0189K09 R, genomic survey sequence.

ACCESSION AZ875430  
 VERSION AZ875430.1 GI:13085433  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0189 row: K column: 09

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0189K09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CCTCAGTC 316  
 |||||  
 Db 18 CCTCAGTC 11

## RESULT 287

AZ942806/c  
 LOCUS AZ942806 19 bp DNA linear GSS 26-APR-2001  
 DEFINITION 2M0203F09F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203F09 F, genomic survey sequence.

ACCESSION AZ942806  
 VERSION AZ942806.1 GI:13806397  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: F column: 09

Seq primer: CGTTGTAACACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

1. .19

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0203F09"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 581 GTACTTTG 588  
|||||  
Db 16 GTACTTTG 9

## RESULT 288

AZ960826

LOCUS

DEFINITION 2M0229H03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0229H03 F, genomic survey sequence.

ACCESSION

AZ960826

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0229 row: H column: 03

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0229H03"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 ATTCAAAA 49  
|||||  
Db 3 ATTCAAAA 10

## RESULT 289

AZ960826/c

LOCUS

DEFINITION 2M0229H03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0229H03 F, genomic survey sequence.

ACCESSION

AZ960826

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0229 row: H column: 03

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0229H03"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 447 TACTTTTG 454  
 |||||  
 Db 13 TACTTTTG 6

## RESULT 290

AZ967656  
 LOCUS 2M0238M03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 DEFINITION clone UUGC2M0238M03 R, genomic survey sequence.

ACCESSION AZ967656  
 VERSION AZ967656.1 GI:13838883  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0238 row: M column: 09  
 Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1..19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0238M09"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 CAAAAATG 52  
 |||||  
 Db 2 CAAAAATG 9

## RESULT 291

AZ977761/C  
 LOCUS 2M0253I16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 DEFINITION clone UUGC2M0253I16 R, genomic survey sequence.

ACCESSION AZ977761  
 VERSION AZ977761.1 GI:13848988  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0253 row: I column: 16  
 Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1..19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0253I16"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 TTGTGAGA 458  
|||||  
Db 15 TTGTGAGA 8

## RESULT 292

AZ983624

LOCUS AZ983624 19 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0264A22R Mouse 10kb plasmid UGC2M library Mus musculus genomic  
clone UGC2M0264A22 R, genomic survey sequence.

ACCESSION AZ983624

VERSION AZ983624.1 GI:13854851

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0264 row: A column: 22  
Seq primer: CACACGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19

## FEATURES

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M0264A22"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 TTATCTTC 148  
|||||  
Db 8 TTATCTTC 15

## RESULT 293

AZ989738/c

LOCUS AZ989738 19 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0273M10F Mouse 10kb plasmid UGC2M library Mus musculus genomic  
clone UGC2M0273M10 F, genomic survey sequence.

ACCESSION AZ989738

VERSION AZ989738.1 GI:13860965

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0273 row: M column: 10  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19

## FEATURES

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M0273M10"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTT 435  
|||||||  
Db 8 ATTATTTT 1

RESULT 294  
AZ990193/c  
LOCUS  
DEFINITION  
2M0273L15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0273L15 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A., and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: L column: 15

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0273L15"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGGAAGGG 492  
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Db 15 GGGGAAGGG 8

RESULT 295  
BH000440/c

## LOCUS

DEFINITION  
2M0288I117F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0288I17 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A., and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: I column: 17

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0288I17"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 AACTTCA 478

Db 15 AACTTCA 8

## RESULT 296

BZ424622 19 bp DNA linear GSS 13-DEC-2002  
LOCUS  
DEFINITION 10016863-4991 Aspergillus terreus random genomic DNA clone library  
Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424622

VERSION BZ424622.1

KEYWORDS GI:26666077

SOURCE GSS.

ORGANISM Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

## REFERENCE

1 (bases 1 to 19)  
Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,  
Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,  
Monreal, A.W., Feibelman, T.P., Mayoraga, M.E., Maxon, M.E., Sykes, K.,  
Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and  
Madden, K.T.

TITLE Integrating transcriptional and metabolite profiles to direct the  
engineering of lovastatin-producing strains

## JOURNAL

## COMMENT

Unpublished (2002)  
Contact: Zimmer DP

Microbia, Inc.

One Kendall Square Building 1400 W, Cambridge, MA 02139, USA

Tel: 617-621-8322

Fax: 617-

Email: dzimmer@microbia.com

Class: plasmid ends.

Location/Qualifiers

1..19

/organism="Aspergillus terreus"

/mol\_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db\_xref="taxon:33178"

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/clone\_lib="Aspergillus terreus random genomic DNA clone

library"

/note="vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;

Sau3A genomic fragments ligated into BamHI digested

pZEROTM-2"

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162

|||||

Db 9 AGAACGGC 2

## RESULT 297

## LOCUS

BZ424949/c

## DEFINITION

100022331-5019 Aspergillus terreus random genomic DNA clone library

Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424949

VERSION BZ424949.1

KEYWORDS GI:26666404

SOURCE GSS.

ORGANISM Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 19)

Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,

Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,

Monreal, A.W., Feibelman, T.P., Mayoraga, M.E., Maxon, M.E., Sykes, K.,

Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and

Madden, K.T.

TITLE Integrating transcriptional and metabolite profiles to direct the

engineering of lovastatin-producing strains

Unpublished (2002)

Contact: Zimmer DP

Microbia, Inc.

One Kendall Square Building 1400 W, Cambridge, MA 02139, USA

Tel: 617-621-8322

Fax: 617-

Email: dzimmer@microbia.com

Class: plasmid ends.

Location/Qualifiers

1..19

/organism="Aspergillus terreus"

/mol\_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db\_xref="taxon:33178"

/lab\_host="Escherichia coli"

/clone\_lib="Aspergillus terreus random genomic DNA clone

library"

/note="vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;

Sau3A genomic fragments ligated into BamHI digested

pZEROTM-2"

## ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.9e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162

|||||

Db 8 AGAACGGC 1

## RESULT 298

## LOCUS

BZ425196/c

## DEFINITION

100026548-5021 Aspergillus terreus random genomic DNA clone library

Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ425196

VERSION BZ425196.1

KEYWORDS GI:26666651

SOURCE GSS.

ORGANISM Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 19)

Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,

Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,

Monreal, A.W., Feibelman, T.P., Mayoraga, M.E., Maxon, M.E., Sykes, K.,

Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and

Madden, K.T.

TITLE Integrating transcriptional and metabolite profiles to direct the



```

engineering of lovastatin-producing strains
Unpublished (2002)
Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
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            /organism="Aspergillus terreus"
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            /lab_host="Escherichia coli"
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            Sau3A genomic fragments ligated into BamHI digested
            pZErOTM-2 "
ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 4.9e+07;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
    |||||
Db 8 AGAACGGC 1

RESULT 300
TA30B01Q/c
LOCUS TA30B01Q 19 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 30b01, reverse sequence,
genomic survey sequence.
ACCESSION AL452860
VERSION AL452860.1 GI:11854424
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
          Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
          Trypanosoma.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
          Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
          Melville,S.E., Raftandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
          project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
          Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
          nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
          Rockville, MD. Genomic DNA isolated from a cloned population of
          Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
          to give a tight size distribution (
          4 kb). The v + i method used for the library construction is
          described in detail in Smith, H. and Venter, J.C. (Making small
          insert libraries for whole genome shotgun sequencing projects. In
          Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
          Barrell, Oxford University Press, 1999).
          Email: neisayed@tigr.org
          Details of T. brucei sequencing at the Sanger Centre are available
          at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
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            /organism="Trypanosoma brucei"
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ORIGIN

Query Match          1.3%; Score 8; DB 29; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GAAGTTTC 34
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Db 18 GAAGTTTC 11

Search completed: March 4, 2004, 23:31:52
Job time : 2297 secs

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```

engineering of lovastatin-producing strains
Unpublished (2002)
Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
    source
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            /organism="Aspergillus terreus"
            /mol_type="genomic DNA"
            /strain="ATCC 20542 (A. terreus Thom, anamorph)"
            /db_xref="taxon:33178"
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            Sau3A genomic fragments ligated into BamHI digested
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    Query Match          1.3%; Score 8; DB 28; Length 19;
    Best Local Similarity 100.0%; Pred. No. 4.9e+07;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGC 162
    |||||
Db 8 AGAACGGC 1

RESULT 299
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LOCUS BZ425408 19 bp DNA linear GSS 13-DEC-2002
DEFINITION 100031441-5051 Aspergillus terreus random genomic DNA clone library
          Aspergillus terreus genomic, genomic survey sequence.
ACCESSION BZ425408
VERSION BZ425408.1 GI:26666863
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
          Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
          Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
          Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
          Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
          Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
          engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
          Microbia, Inc.
          One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
          Tel: 617-621-8322
          Fax: 617-
          Email: dzimmer@microbia.com
          Class: plasmid ends.
FEATURES
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            /mol_type="genomic DNA"
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            /clone_lib="Aspergillus terreus random genomic DNA clone
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            /note="Vector: pZErOTM-2; Site 1: Sau3A; Site 2: BamHI;
            Sau3A genomic fragments ligated into BamHI digested
            pZErOTM-2 "
ORIGIN

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 4, 2004, 23:34:18 ; Search time 3736 Seconds

(without alignments)

2297.088 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198

Sequence: 1 MDSLLMNRKFLYQFNVRW.....ILLPLYEVDDLDAFRILGL 198

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 1

Total number of hits satisfying chosen parameters: 687819

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPTO.spool/US09966880/runat\_04032004\_083152\_22387/app.query.fasta\_1.391  
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-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20  
-USER=US09966880@cgn.1.1.3731 @runat\_04032004\_083152\_22387 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
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21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

29: em.vi.\*  
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34: em.htg.pln.\*  
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36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	6	3.0	18	6	AR300029	Sequence
C 2	6	3.0	19	6	AR295883	Sequence
3	6	3.0	20	6	AR026495	Sequence
C 4	6	3.0	20	6	AR224722	Sequence
5	6	3.0	20	6	AR297575	Sequence
6	6	3.0	20	6	AR314839	Sequence
7	5	2.5	15	6	AR180659	Sequence
C 8	5	2.5	16	6	AX322719	Sequence
9	5	2.5	17	6	A35587	Synthetic h
C 10	5	2.5	17	6	A45700	Sequence 31
C 11	5	2.5	17	6	AR039735	Sequence
C 12	5	2.5	17	6	AR039737	Sequence
13	5	2.5	17	6	AR057431	Sequence
14	5	2.5	17	6	AR057487	Sequence
15	5	2.5	17	6	AR057687	Sequence
16	5	2.5	17	6	AR057777	Sequence
17	5	2.5	17	6	AR057782	Sequence
18	5	2.5	17	6	AR115189	Sequence
19	5	2.5	17	6	AR115245	Sequence
20	5	2.5	17	6	AR115445	Sequence
21	5	2.5	17	6	AR115535	Sequence
22	5	2.5	17	6	AR115540	Sequence
23	5	2.5	17	6	BD241216	Methods a
C 24	5	2.5	17	6	BD256674	Regulatio
25	5	2.5	17	6	AR186522	Sequence
26	5	2.5	17	6	AR186523	Sequence
27	5	2.5	17	6	AR188866	Sequence
28	5	2.5	17	6	AR188867	Sequence
29	5	2.5	17	6	AR188868	Sequence
30	5	2.5	17	6	AR191815	Sequence
31	5	2.5	17	6	AR191816	Sequence
C 32	5	2.5	17	6	AR193560	Sequence
33	5	2.5	17	6	AR285974	Sequence
34	5	2.5	17	6	AR232153	Sequence
35	5	2.5	17	6	AR323154	Sequence
36	5	2.5	17	6	AR324719	Sequence
37	5	2.5	17	6	AR324720	Sequence
38	5	2.5	17	6	AR324721	Sequence
39	5	2.5	17	6	AR325710	Sequence
40	5	2.5	17	6	AR325711	Sequence
41	5	2.5	17	6	AR327446	Sequence
42	5	2.5	17	6	AR397964	Sequence
C 43	5	2.5	17	6	AX214940	Sequence
C 44	5	2.5	17	6	AX215777	Sequence
C 45	5	2.5	17	6	AX215821	Sequence

ALIGNMENTS

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LOCUS              Sequence 11764 from patent US 6537751.
DEFINITION
ACCESSION          AR300029
VERSION            AR300029.1  GI:31687313
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 18)
AUTHORS             Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE               Biallelic markers for use in constructing a high density
JOURNAL             Patent: US 6537751-A 11764 25-MAR-2003;
FEATURES            Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
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Best Local Similarity: 100.00%    Indels:       0
Query Match:           3.03%      Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AR300029 (1-18)

QY      179 IleLeuLeuProLeuTyr 184
Db      1 ATCCTTCTCCACTCTAC 18

RESULT 2
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LOCUS              AR295883          19 bp  DNA          linear  PAT 12-JUN-2003
DEFINITION          Sequence 7618 from patent US 6537751.
ACCESSION          AR295883
VERSION            AR295883.1  GI:31683167
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 19)
AUTHORS             Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE               Biallelic markers for use in constructing a high density
JOURNAL             Patent: US 6537751-A 7618 25-MAR-2003;
FEATURES            Location/Qualifiers
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ORIGIN
Alignment Scores:      744      Length:      19
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches:  0
Best Local Similarity: 100.00%    Indels:       0
Query Match:           3.03%      Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AR295883 (1-19)

QY      167 GluAsnSerValArgLeu 172
Db      19 GAAATAAGTGTAAAGCTC 2

RESULT 3
AR026495
LOCUS              AR026495          20 bp  DNA          linear  PAT 29-SEP-1999
DEFINITION          Sequence 2 from patent US 5856099.

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ACCESSION          AR026495
VERSION            AR026495.1  GI:5937335
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 20)
AUTHORS             Miraglia,L., Bennett,C.Frank., Dean,N. and Geiger,T.
TITLE               Antisense compositions and methods for modulating type I
JOURNAL             interleukin-1 receptor expression
FEATURES            Patent: US 5856099-A 2 05-JAN-1999;
                     Location/Qualifiers
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:      778      Length:      20
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches:  0
Best Local Similarity: 100.00%    Indels:       0
Query Match:           3.03%      Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AR026495 (1-20)

QY      125 GlyLeuArgArgLeuHis 130
Db      2 GGCCTGCGCGCTCCAC 19

RESULT 4
AR224722/c
LOCUS              AR224722          20 bp  DNA          linear  PAT 26-SEP-2002
DEFINITION          Sequence 27 from patent US 6440739.
ACCESSION          AR224722
VERSION            AR224722.1  GI:23333562
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 20)
AUTHORS             Bennett,C.F. and Freier,S.M.
TITLE               Antisense modulation of glioma-associated oncogene-2 expression
JOURNAL             Patent: US 6440739-A 27 27-AUG-2002;
FEATURES            Location/Qualifiers
                     1..20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
Alignment Scores:      778      Length:      20
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches:  0
Best Local Similarity: 100.00%    Indels:       0
Query Match:           3.03%      Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AR224722 (1-20)

QY      122 GluProGlyLeuArg 127
Db      18 GAGCCTGAGGCGCTCGG 1

RESULT 5
AR297575
LOCUS              AR297575          20 bp  DNA          linear  PAT 12-JUN-2003
DEFINITION          Sequence 9310 from patent US 6537751.
ACCESSION          AR297575
VERSION            AR297575.1  GI:31684859
KEYWORDS
SOURCE             Unknown.

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ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE          Biallelic markers for use in constructing a high density
               disequilibrium map of the human genome
JOURNAL        Patent: US 6537751-A 9310 25-MAR-2003;
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:      778      Length:      20
Score:          6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    3.03%      Indels:      0
DB:             6         Gaps:        0
US-09-966-880A-8 (1-198) x AR297575 (1-20)
QY             40 ThrSerPheSerLeuAsp 45
Db             2 ACAGTTTCTCATTAGAC 19
RESULT 6
LOCUS          AR314839      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION     Sequence 5376 from patent US 6559294.
ACCESSION      AR314839
VERSION        AR314839.1 GI:31708265
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffiths,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
               Sankaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 5376 06-MAY-2003;
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:      778      Length:      20
Score:          6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    3.03%      Indels:      0
DB:             6         Gaps:        0
US-09-966-880A-8 (1-198) x AR314839 (1-20)
QY             167 GluAsnSerValArgLeu 172
Db             1 GAGAACTCGTGGCGCTG 18
RESULT 7
AR180659
LOCUS          AR180659      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION     Sequence 727 from patent US 6331152.
ACCESSION      AR180659
VERSION        AR180659.1 GI:20222692
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Unclassified.
TITLE          Unclassified.
AUTHORS        Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE          Gene expression profiles in normal and cancer cells
JOURNAL        Patent: US 6331152-A 727 25-DEC-2001;
FEATURES       Location/Qualifiers
               source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      7.11e+03      Length:      15
Score:          5.00     Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             6         Gaps:        0
US-09-966-880A-8 (1-198) x AR180659 (1-15)
QY             93 HisValAlaAspPhe 97
Db             1 CATGTTGCTGACTTT 15
RESULT 8
AX322719/c
LOCUS          AX322719      16 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION     Sequence 4 from Patent WO0192502.
ACCESSION      AX322719
VERSION        AX322719.1 GI:18093709
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1
AUTHORS        Svendsen,A., Glad,S.O., Fukuyama,S. and Matsui,T.
TITLE          Cutinase variants
JOURNAL        Patent: WO 0192502-A 4 06-DEC-2001;
FEATURES       Location/Qualifiers
               source
               1..16
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               /note="Dop2-R"
ORIGIN
Alignment Scores:
Pred. No.:      7.52e+03      Length:      16
Score:          5.00     Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             6         Gaps:        0
US-09-966-880A-8 (1-198) x AX322719 (1-16)
QY             70 LeuAspProGlyArg 74
Db             16 CTGGATCCAGGCGT 2
RESULT 9
AR35587
LOCUS          A35587      17 bp      DNA      linear      PAT 02-DEC-1996
DEFINITION     Synthetic human IFN-alpha 2 gene oligo.
ACCESSION      A35587
VERSION        A35587.1 GI:1926969
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1 (bases 1 to 17)
AUTHORS        Camble,R. and Edge,M.D.
TITLE          Analogous interferon polypeptides, process for their preparation

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and pharmaceutical compositions containing them  
Patent: EP 0194006-A 32 10-SEP-1986;  
IMPERIAL CHEMICAL INDUSTRIES PLC

## JOURNAL

source

1. .17

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A35587 (1-17)

Qy 157 ArgThrPheLysAla 161

Db 2 AGACGTTTAAGGCG 16

RESULT 10

A45700/c

LOCUS

DEFINITION Sequence 31 from Patent WO9520053.

ACCESSION A45700

VERSION A45700.1 GI:2300089

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other publication AU 1459595 950808.

Medical Res Council (GB)

Location/Qualifiers

1. .17

/organism="unidentified"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A45700 (1-17)

Qy 104 LeuSerLeuArgIle 108

Db 15 CTTTCACTCGGAAT 1

RESULT 11

AR039735/c

LOCUS

DEFINITION Sequence 583 from patent US 5807743.

ACCESSION AR039735

VERSION AR039735.1 GI:5959098

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Stinchcomb, D.T. and McSwiggen, J.A.

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039735 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 17 GAAGGACTTAAAGG 3

RESULT 12

AR039737/c

LOCUS

DEFINITION Sequence 585 from patent US 5807743.

ACCESSION AR039737

VERSION AR039737.1 GI:5959100

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5807743-A 583 15-SEP-1998;

Location/Qualifiers

1. .17

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039735 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 17 GAAGGACTTAAAGG 3

RESULT 13

AR057431

LOCUS

DEFINITION Sequence 1635 from patent US 5837542.

ACCESSION AR057431

VERSION AR057431.1 GI:5983008

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5837542-A 1635 17-NOV-1998;

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039737 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 16 GAAGGACTTAAAGG 2

RESULT 13

AR057431

LOCUS

DEFINITION Sequence 1635 from patent US 5837542.

ACCESSION AR057431

VERSION AR057431.1 GI:5983008

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5837542-A 1635 17-NOV-1998;

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039737 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 16 GAAGGACTTAAAGG 2

RESULT 13

AR057431

LOCUS

DEFINITION Sequence 1635 from patent US 5837542.

ACCESSION AR057431

VERSION AR057431.1 GI:5983008

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5837542-A 1635 17-NOV-1998;

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039737 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 16 GAAGGACTTAAAGG 2

RESULT 13

AR057431

LOCUS

DEFINITION Sequence 1635 from patent US 5837542.

ACCESSION AR057431

VERSION AR057431.1 GI:5983008

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5837542-A 1635 17-NOV-1998;

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039737 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 16 GAAGGACTTAAAGG 2

RESULT 13

AR057431

LOCUS

DEFINITION Sequence 1635 from patent US 5837542.

ACCESSION AR057431

VERSION AR057431.1 GI:5983008

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Interleukin-2 receptor gamma-chain ribozymes

Patent: US 5837542-A 1635 17-NOV-1998;

Location/Qualifiers

1. .17

/organism="unassigned DNA"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR0

ORIGIN	/organism="unknown"	/mol_type="unassigned DNA"
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057431 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGCTCTTCCTC 15	
RESULT 14		
AR057487		
LOCUS	AR057487	17 bp DNA
DEFINITION	Sequence 1691 from patent US 5837542.	linear
ACCESSION	AR057487	
VERSION	AR057487.1	
KEYWORDS	GI:5983064	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1691 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057487 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGCTCTTCCTC 15	
RESULT 15		
AR057687		
LOCUS	AR057687	17 bp DNA
DEFINITION	Sequence 1891 from patent US 5837542.	linear
ACCESSION	AR057687	
VERSION	AR057687.1	
KEYWORDS	GI:5983264	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1891 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057687 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGCTCTTCCTC 15	
RESULT 16		
AR057777		
LOCUS	AR057777	17 bp DNA
DEFINITION	Sequence 1981 from patent US 5837542.	linear
ACCESSION	AR057777	
VERSION	AR057777.1	
KEYWORDS	GI:5983354	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1981 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057777 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGCTCTTCCTC 15	
RESULT 17		
AR057782		
LOCUS	AR057782	17 bp DNA
DEFINITION	Sequence 1986 from patent US 5837542.	linear
ACCESSION	AR057782	
VERSION	AR057782.1	
KEYWORDS	GI:5983359	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1986 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	

ORIGIN	/organism="unknown"	/mol_type="unassigned DNA"
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057431 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGTGCTCTTCCTC 15	
RESULT 14		
AR057487		
LOCUS	AR057487	17 bp DNA
DEFINITION	Sequence 1691 from patent US 5837542.	linear
ACCESSION	AR057487	
VERSION	AR057487.1	
KEYWORDS	GI:5983064	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1691 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057487 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGTGCTCTTCCTC 15	
RESULT 15		
AR057687		
LOCUS	AR057687	17 bp DNA
DEFINITION	Sequence 1891 from patent US 5837542.	linear
ACCESSION	AR057687	
VERSION	AR057687.1	
KEYWORDS	GI:5983264	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1891 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057687 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGTGCTCTTCCTC 15	
RESULT 16		
AR057777		
LOCUS	AR057777	17 bp DNA
DEFINITION	Sequence 1981 from patent US 5837542.	linear
ACCESSION	AR057777	
VERSION	AR057777.1	
KEYWORDS	GI:5983354	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1981 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.53%	Indels: 0
DB:	6	Gaps: 0
US-09-966-880A-8 (1-198) x AR057777 (1-17)		
Qy	58 GluLeuLeuPheLeu 62	
Db	1 GAACGTGCTCTTCCTC 15	
RESULT 17		
AR057782		
LOCUS	AR057782	17 bp DNA
DEFINITION	Sequence 1986 from patent US 5837542.	linear
ACCESSION	AR057782	
VERSION	AR057782.1	
KEYWORDS	GI:5983359	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes	
JOURNAL	Patent: US 5837542-A 1986 17-NOV-1998;	
FEATURES	Location/Qualifiers	
source	1..17	
ORIGIN	/organism="unknown"	
/mol_type="unassigned DNA"		
Alignment Scores:		
Pred. No.:	7.93e+03	Length: 17
Score:	5.00	Matches: 5
Percent Similarity:	100.00%	

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR057782 (1-17)

Qy 58 GluLeuLeuPheLeu 62  
Db 1 GAACTGCTCTTCCTC 15

RESULT 18  
AR115189  
LOCUS AR115189 linear PAT 16-MAY-2001  
DEFINITION Sequence 1635 from patent US 6132967.  
ACCESSION AR115189  
VERSION AR115189.1 GI:14095511  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1635 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115189 (1-17)

Qy 58 GluLeuLeuPheLeu 62  
Db 1 GAACTGCTCTTCCTC 15

RESULT 19  
AR115245  
LOCUS AR115245 linear PAT 16-MAY-2001  
DEFINITION Sequence 1691 from patent US 6132967.  
ACCESSION AR115245  
VERSION AR115245.1 GI:14095567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1691 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115245 (1-17)

Qy 58 GluLeuLeuPheLeu 62  
Db 1 GAACTGCTCTTCCTC 15

RESULT 20  
AR115445  
LOCUS AR115445 linear PAT 16-MAY-2001  
DEFINITION Sequence 1891 from patent US 6132967.  
ACCESSION AR115445  
VERSION AR115445.1 GI:14095767  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1891 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115445 (1-17)

Qy 58 GluLeuLeuPheLeu 62  
Db 1 GAACTGCTCTTCCTC 15

RESULT 21  
AR115535  
LOCUS AR115535 linear PAT 16-MAY-2001  
DEFINITION Sequence 1981 from patent US 6132967.  
ACCESSION AR115535  
VERSION AR115535.1 GI:14095857  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1981 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0

FT	source	1..17	/organism='Homo sapiens (human)'
FT	FT	Location/Qualifiers	
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		/mol_type='genomic DNA'	
		/db_xref='taxon:9606'	
ORIGIN			
Alignment Scores:			
Pred. No.:	7.93e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0
US-09-966-880A-8 (1-198) x BD241216 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x AR115540 (1-17)			
QY	58 GluLeuLeuPheLeu 62		
DB	1 GAACGTGCTTCTCCTC 15		
RESULT 22			
AR115540			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x AR115535 (1-17)			
QY	58 GluLeuLeuPheLeu 62		
DB	1 GAACGTGCTTCTCCTC 15		
RESULT 23			
BD241216			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuser 173		
DB	3 ACGTCCGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			



```

QY      11 PheLeuTyGlnPhe 15
Db      15 TTTCCTCATCAGTTC 1

RESULT 25
AR186522
LOCUS   Sequence 2010 from patent US 6346398.
DEFINITION
ACCESSION AR186522
VERSION   AR186522.1 GI:20232487
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6346398-A 2010 12-FEB-2002;
FEATURES
    source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR186522 (1-17)

QY      102 ProAsnLeuSerLeu 106
Db      3 CCGAATCTATCTTTG 17

RESULT 26
AR186523
LOCUS   Sequence 2011 from patent US 6346398.
DEFINITION
ACCESSION AR186523
VERSION   AR186523.1 GI:20232488
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6346398-A 2011 12-FEB-2002;
FEATURES
    source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR186523 (1-17)

QY      102 ProAsnLeuSerLeu 106
Db      1 CCGAATCTATCTTTG 15

RESULT 27
AR188866
LOCUS   Sequence 4354 from patent US 6346398.
DEFINITION
ACCESSION AR188866
VERSION   AR188866.1 GI:20234831
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6346398-A 4354 12-FEB-2002;
FEATURES
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    1..17
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    /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR188866 (1-17)

QY      157 ArgThrPhelysala 161
Db      3 AGAACTTTTAAAGCT 17

RESULT 28
AR188867
LOCUS   Sequence 4355 from patent US 6346398.
DEFINITION
ACCESSION AR188867
VERSION   AR188867.1 GI:20234832
KEYWORDS
SOURCE   Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6346398-A 4355 12-FEB-2002;
FEATURES
    source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR188867 (1-17)

QY      157 ArgThrPhelysala 161
Db      2 AGAACTTTTAAAGCT 16

RESULT 29
AR188868

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LOCUS AR188868 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4356 from patent US 6346398.  
ACCESSION AR188868  
VERSION AR188868.1 GI:20234833  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 4356 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
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ORIGIN  
Alignment Scores: 7.93e+03 Length: 17  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR188868 (1-17)  
QY 157 ArgThrPhelysala 161  
Db 1 AGAACTTTTAAAGCT 15  
RESULT 30  
AR191815  
LOCUS AR191815 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 7303 from patent US 6346398.  
ACCESSION AR191815  
VERSION AR191815.1 GI:20237780  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7303 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
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/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores: 7.93e+03 Length: 17  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR191815 (1-17)  
QY 179 IleLeuLeuProLeu 183  
Db 2 ATACTCTTACCCTG 16  
RESULT 31  
AR191816  
LOCUS AR191816 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 7304 from patent US 6346398.  
ACCESSION AR191816

VERSION AR191816.1 GI:20237781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7304 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores: 7.93e+03 Length: 17  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR191816 (1-17)  
QY 179 IleLeuLeuProLeu 183  
Db 1 ATACTCTTACCCTG 15  
RESULT 32  
AR193560/c  
LOCUS AR193560 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 31 from patent US 6348313.  
ACCESSION AR193560  
VERSION AR193560.1 GI:20240152  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sibson,D.Koss.  
TITLE Sequencing of nucleic acids  
JOURNAL Patent: US 6348313-A 31 19-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores: 7.93e+03 Length: 17  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR193560 (1-17)  
QY 104 LeuSerLeuArgIle 108  
Db 15 CTTTCACTCCGATT 1  
RESULT 33  
AR285974  
LOCUS AR285974 17 bp RNA linear PAT 10-APR-2003  
DEFINITION Sequence 346 from patent US 6528640.  
ACCESSION AR285974  
VERSION AR285974.1 GI:29723570  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 17)  
Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
Synthetic ribonucleic acids with RNase activity  
Patent: US 6528640-A 346 04-MAR-2003;  
Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR285974 (1-17)

Qy 89 AspCysalaarghis 93  
Db 3 GATTGTGCGAGGCAC 17

RESULT 34  
AR323153  
LOCUS AR323153 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 555 from patent US 6566127.  
ACCESSION AR323153  
VERSION AR323153.1 GI:33708961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 555 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AR323153 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
Db 3 CCGAATCTATCTTTG 17

RESULT 35  
AR323154  
LOCUS AR323154 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 556 from patent US 6566127.  
ACCESSION AR323154  
VERSION AR323154.1 GI:33708962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 556 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"<

FEATURES	source	Location/Qualifiers	1. .17	/organism="unknown"	/mol_type="unassigned RNA"
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR324720 (1-17)					
QY	157 ArgThrPhelysAla 161				
Db	2 AGAAGCTTTAAAGCT 16				
RESULT 38					
AR324721					
LOCUS	AR324721	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 2123 from patent US 6566127.				
ACCESSION	AR324721				
VERSION	AR324721.1 GI:33710529				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 3112 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR324721 (1-17)					
QY	157 ArgThrPhelysAla 161				
Db	1 AGAAGCTTTAAAGCT 15				
RESULT 39					
AR325710					
LOCUS	AR325710	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 3112 from patent US 6566127.				
ACCESSION	AR325710				
VERSION	AR325710.1 GI:33711518				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 3112 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR325711 (1-17)					
QY	179 IleLeuLeuProLeu 183				
Db	1 ATACTCTTACCCTG 15				
RESULT 41					
AR327446					
LOCUS	AR327446	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 4848 from patent US 6566127.				
ACCESSION	AR327446				
VERSION	AR327446.1 GI:33713254				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 4848 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR327446 (1-17)

Qy 102 ProAsnLeuSerLeu 106  
 Db 2 CCGAATCTATCTTG 16

# RESULT 42

AR397964  
 LOCUS AX397964 17 bp RNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 345 from patent US 6617438.  
 ACCESSION AR397964  
 VERSION AR397964.1 GI:40135388  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 17)  
 Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
 Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
 Oligoribonucleotides with enzymatic activity  
 JOURNAL Patent: US 6617438-A 345 09-SEP-2003;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

# ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR397964 (1-17)

Qy 89 AspCysAlaArgHis 93  
 Db 3 GATTGTGGAGGCAC 17

# RESULT 43

AX214940/c  
 LOCUS AX214940 17 bp RNA linear PAT 07-SEP-2001  
 DEFINITION Sequence 382 from Patent WO0159103.  
 ACCESSION AX214940  
 VERSION AX214940.1 GI:15524983  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

# REFERENCE

1 Blatt,L., McSwiggen,J. and Chowrira,B.M.  
 Method and reagent for the modulation and diagnosis of cd20 and  
 nogo gene expression  
 JOURNAL Patent: WO 0159103-A 382 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

# FEATURES

source 1..17  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

# ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX214940 (1-17)

Qy 169 SerValArgLeuSer 173  
 Db 16 TCAGTGAGACTTCT 2

# RESULT 44

AX215777/c  
 LOCUS AX215777 17 bp RNA linear PAT 07-SEP-2001  
 DEFINITION Sequence 1219 from Patent WO0159103.  
 ACCESSION AX215777  
 VERSION AX215777.1 GI:15525820  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

# REFERENCE

1 Blatt,L., McSwiggen,J. and Chowrira,B.M.  
 Method and reagent for the modulation and diagnosis of cd20 and  
 nogo gene expression  
 JOURNAL Patent: WO 0159103-A 1219 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

# FEATURES

source 1..17  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

# ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215777 (1-17)

Qy 58 GluLeuLeuPheLeu 62  
 Db 16 GAGCTTCTGTTCTT 2

# RESULT 45

AX215821/c  
 LOCUS AX215821 17 bp RNA linear PAT 07-SEP-2001  
 DEFINITION Sequence 1263 from Patent WO0159103.  
 ACCESSION AX215821  
 VERSION AX215821.1 GI:15525864  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

# REFERENCE

1 Blatt,L., McSwiggen,J. and Chowrira,B.M.  
 Method and reagent for the modulation and diagnosis of cd20 and  
 nogo gene expression  
 JOURNAL Patent: WO 0159103-A 1263 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

# FEATURES

source 1..17  
 Location/Qualifiers



## artificial sequences.

```

REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2555 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
source
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX217113 (1-17)
QY 58 GlulLeuLeuPheLeu 62
Db 15 GAGCTTCTGTTCTTT 1
RESULT 50
AX264024
LOCUS AX264024 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1415 from Patent WO0173002.
ACCESSION AX264024
VERSION AX264024.1 GI:16512823
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 1415 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
source
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX264024 (1-17)
QY 129 LeuHisArgAlaGly 133
Db 2 CTGCACCGGCGCGG 16
RESULT 51
AX264025/c
LOCUS AX264025/c 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1416 from Patent WO0173002.
ACCESSION AX264025

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VERSION AX264025.1 GI:16512824
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 1416 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
source
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX264025 (1-17)
QY 129 LeuHisArgAlaGly 133
Db 16 CTGCACCGGCGCGG 2
RESULT 52
AX2666427/c
LOCUS AX2666427/c 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3818 from Patent WO0173002.
ACCESSION AX2666427
VERSION AX2666427.1 GI:16515226
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 3818 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
source
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX2666427 (1-17)
QY 93 HisValAlaAspPhe 97
Db 15 CATGTTGCAGACTTT 1
RESULT 53
AX2666428

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LOCUS       AX266428                      17 bp    DNA
DEFINITION   Sequence 3819 from Patent WO0173002.
ACCESSION    AX266428
VERSION      AX266428.1  GI:16515227
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
              stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 3819 04-OCT-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%          Indels:        0
DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AX266428 (1-17)

QY          93 HisValAlaAspPhe 97
DB          3 CATGTTGCAGACTTT 17

RESULT 54
LOCUS       AX280085                      17 bp    DNA
DEFINITION   Sequence 14 from Patent WO0177295.
ACCESSION    AX280085
VERSION      AX280085.1  GI:16607527
KEYWORDS     Aspergillus fumigatus
SOURCE       Aspergillus fumigatus
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
              Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE    1
AUTHORS      Denning,D.W., Brookman,J.L., Rickers,A. and Birch,M.
TITLE        Mutant bank
JOURNAL      Patent: WO 0177295-A 14 18-OCT-2001;
              F2G Limited (GB)
FEATURES     source
              1..17
              /organism="Aspergillus fumigatus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:5085"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%          Indels:        0
DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AX280085 (1-17)

QY          175 LeuAtcArgIleIeu 180
DB          3 TTGAGCGCAATTC TC 17

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RESULT 55
LOCUS       AX324869/c                    17 bp    DNA
DEFINITION   Sequence 1007 from Patent WO0192512.
ACCESSION    AX324869
VERSION      AX324869.1  GI:18095623
KEYWORDS     Arabidopsis thaliana (thale cress)
SOURCE       Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE        Targeted chromosomal genomic alterations in plants using modified
              single stranded oligonucleotides
JOURNAL      Patent: WO 0192512-A 1007 06-DEC-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Arabidopsis thaliana"
              /mol_type="unassigned DNA"
              /db_xref="taxon:3702"

ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%          Indels:        0
DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AX324869 (1-17)

QY          32 ValVallyeArgArg 36
DB          15 GTTGTCAAAGGAGA 1

RESULT 56
LOCUS       AX324870                      17 bp    DNA
DEFINITION   Sequence 1008 from Patent WO0192512.
ACCESSION    AX324870
VERSION      AX324870.1  GI:18095624
KEYWORDS     Arabidopsis thaliana (thale cress)
SOURCE       Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE        Targeted chromosomal genomic alterations in plants using modified
              single stranded oligonucleotides
JOURNAL      Patent: WO 0192512-A 1008 06-DEC-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Arabidopsis thaliana"
              /mol_type="unassigned DNA"
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ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%          Indels:        0
DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AX324870 (1-17)

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QY      32 ValVallysArgArg 36
DB      3 GTTGTCARAAGGAGA 17

RESULT 57
LOCUS   AX325133              17 bp  DNA
DEFINITION
Sequence 1271 from Patent WO0192512.
ACCESSION
AX325133
VERSION
AX325133.1 GI:18095888
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1271 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      3 CGACTGAGTCGTCAG 17

RESULT 58
LOCUS   AX325134/C           17 bp  DNA
DEFINITION
Sequence 1272 from Patent WO0192512.
ACCESSION
AX325134
VERSION
AX325134.1 GI:18095889
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1272 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      3 CGACTGAGTCGTCAG 17

RESULT 59
LOCUS   AX499899              17 bp  DNA
DEFINITION
Sequence 1206 from Patent EP1229046.
ACCESSION
AX499899
VERSION
AX499899.1 GI:23382192
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1206 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      172 LeuSerArgGlnLeu 176
DB      3 CTTTCAGACACTG 17

RESULT 60
LOCUS   AX499900              17 bp  DNA
DEFINITION
Sequence 1207 from Patent EP1229046.
ACCESSION
AX499900
VERSION
AX499900.1 GI:23382193
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1207 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      3 CGACTGAGTCGTCAG 17

RESULT 61
LOCUS   AX325133              17 bp  DNA
DEFINITION
Sequence 1271 from Patent WO0192512.
ACCESSION
AX325133
VERSION
AX325133.1 GI:18095888
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1271 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      3 CGACTGAGTCGTCAG 17

RESULT 62
LOCUS   AX325134/C           17 bp  DNA
DEFINITION
Sequence 1272 from Patent WO0192512.
ACCESSION
AX325134
VERSION
AX325134.1 GI:18095889
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1272 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      3 CGACTGAGTCGTCAG 17

RESULT 63
LOCUS   AX499899              17 bp  DNA
DEFINITION
Sequence 1206 from Patent EP1229046.
ACCESSION
AX499899
VERSION
AX499899.1 GI:23382192
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1206 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      172 LeuSerArgGlnLeu 176
DB      3 CTTTCAGACACTG 17

RESULT 64
LOCUS   AX499900              17 bp  DNA
DEFINITION
Sequence 1207 from Patent EP1229046.
ACCESSION
AX499900
VERSION
AX499900.1 GI:23382193
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1207 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

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Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 6  
 Gaps: 0

Score: 5.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 6  
 Gaps: 0

US-09-966-880A-8 (1-198) x AX499900 (1-17)

QY 172 LeuSerArgGlnLeu 176  
 DB 2 CTTTCAGCACTG 16

RESULT 61  
 AX499901  
 LOCUS AX499901 17 bp DNA linear PAT 27-SEP-2002  
 DEFINITION Sequence 1208 from Patent EP1229046.  
 ACCESSION AX499901  
 VERSION AX499901.1 GI:23382194  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Zhan, J.  
 TITLE Human testis expressed patched like protein  
 JOURNAL Patent: EP 1229046-A 1208 07-AUG-2002;  
 Aeomica, Inc. (US)

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 6  
 Gaps: 0

US-09-966-880A-8 (1-198) x AX499901 (1-17)

QY 172 LeuSerArgGlnLeu 176  
 DB 1 CTTTCAGCACTG 15

RESULT 62  
 AX531951  
 LOCUS AX531951 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 1460 from Patent EP1239051.  
 ACCESSION AX531951  
 VERSION AX531951.1 GI:25255672  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Shannon, M.  
 TITLE Human posh-like protein 1  
 JOURNAL Patent: EP 1239051-A 1460 11-SEP-2002;  
 Aeomica, Inc. (US)

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17

US-09-966-880A-8 (1-198) x AX531951 (1-17)

QY 21 AlalysGlyArgArg 25  
 DB 3 GCAAAAGGGAGAGG 17

RESULT 63  
 AX531952  
 LOCUS AX531952 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 1461 from Patent EP1239051.  
 ACCESSION AX531952  
 VERSION AX531952.1 GI:25255673  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Shannon, M.  
 TITLE Human posh-like protein 1  
 JOURNAL Patent: EP 1239051-A 1461 11-SEP-2002;  
 Aeomica, Inc. (US)

FEATURES  
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 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7.93e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 6  
 Gaps: 0

US-09-966-880A-8 (1-198) x AX531952 (1-17)

QY 21 AlalysGlyArgArg 25  
 DB 2 GCAAAAGGGAGAGG 16

RESULT 64  
 AX531953  
 LOCUS AX531953 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 1462 from Patent EP1239051.  
 ACCESSION AX531953  
 VERSION AX531953.1 GI:25255675  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Shannon, M.  
 TITLE Human posh-like protein 1  
 JOURNAL Patent: EP 1239051-A 1462 11-SEP-2002;  
 Aeomica, Inc. (US)

FEATURES  
 source  
 1..17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:

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Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX51953 (1-17)

QY 21 AlalysglvArg 25
Db 1 GCATAAGGAGAGG 15

RESULT 65
AX578371/c
LOCUS AX578371 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 209 from Patent WO0211674.
ACCESSION AX578371
VERSION AX578371.1 GI:27647573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 209 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX578371 (1-17)

QY 126 LeuArgLeuHis 130
Db 16 CTTCGGAGATTGCAT 2

RESULT 66
AX578929/c
LOCUS AX578929 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 767 from Patent WO0211674.
ACCESSION AX578929
VERSION AX578929.1 GI:27648131
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 767 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX578929 (1-17)

QY 103 AsnLeuSerLeuArg 107
Db 15 AACTTGCTCTGAGA 1

RESULT 68
AX580320/c
LOCUS AX580320 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2158 from Patent WO0211674.
ACCESSION AX580320
VERSION AX580320.1 GI:27649522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
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source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
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Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX578929 (1-17)

QY 126 LeuArgLeuHis 130
Db 15 CTTCGGAGATTGCAT 1

RESULT 67
AX579988/c
LOCUS AX579988 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1826 from Patent WO0211674.
ACCESSION AX579988
VERSION AX579988.1 GI:27649190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1826 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX579988 (1-17)

QY 103 AsnLeuSerLeuArg 107
Db 15 AACTTGCTCTGAGA 1

RESULT 68
AX580320/c
LOCUS AX580320 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2158 from Patent WO0211674.
ACCESSION AX580320
VERSION AX580320.1 GI:27649522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
```

TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)  
JOURNAL Patent: WO 0211674-A 2158 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)

FEATURES  
source 1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX580320 (1-17)

QY 103 AsnLeuSerLeuArg 107  
Db 16 AACTGCTCTGAGA 2

RESULT 69  
AX634492  
LOCUS AX634492 17 bp RNA linear PAT 21-FEB-2003

DEFINITION Sequence 1631 from Patent EP1260586.

ACCESSION AX634492

VERSION AX634492.1 GI:28470106

KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,

Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related

genes

JOURNAL Patent: EP 1260586-A 1631 27-NOV-2002;

RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
source 1. .17  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634492 (1-17)

QY 58 GluLeuLeuPheLeu 62  
Db 1 GAACGCTCTTCCTC 15

RESULT 70  
AX634523  
LOCUS AX634523 17 bp RNA linear PAT 21-FEB-2003

DEFINITION Sequence 1662 from Patent EP1260586.

ACCESSION AX634523

VERSION AX634523.1 GI:28470137  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,  
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related

genes

JOURNAL Patent: EP 1260586-A 1662 27-NOV-2002;

RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
source 1. .17  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634523 (1-17)

QY 58 GluLeuLeuPheLeu 62

Db 1 GAACGCTCTTCCTC 15

RESULT 71  
AX634727

LOCUS AX634727 17 bp RNA linear PAT 21-FEB-2003

DEFINITION Sequence 1866 from Patent EP1260586.

ACCESSION AX634727

VERSION AX634727.1 GI:28470341

KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified

REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,

Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related

genes

JOURNAL Patent: EP 1260586-A 1866 27-NOV-2002;

RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
source 1. .17  
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ORIGIN

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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634727 (1-17)

Pred. No.:	7.93e+03	Length:	17
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QY	58 GluLeuPheLeu 62	DNA	linear
Db	1 GAACGCTCTTCCTC 15		
RESULT 74			
LOCUS	AX671739	17 bp	DNA
DEFINITION	Sequence 184 from Patent WO03004526.		
ACCESSION	AX671739		
VERSION	AX671739.1 GI:29330087		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
JOURNAL	Telerman,A., Amson,R. and Tuijnder,M.		
FEATURES	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines		
ORIGIN	Patent: WO 03004526-A 184 16-JAN-2003;		
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QY	173 SerArgGlnLeuArg 177	DNA	linear
Db	3 TCAAGGCAGCTGAGA 17		
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LOCUS	AX673136	17 bp	DNA
DEFINITION	Sequence 1581 from Patent WO03004526.		
ACCESSION	AX673136		
VERSION	AX673136.1 GI:29331484		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
JOURNAL	Telerman,A., Amson,R. and Tuijnder,M.		
FEATURES	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines		
ORIGIN	Patent: WO 03004526-A 1581 16-JAN-2003;		
Alignment Scores:	Molecular Engines Laboratories (FR)		
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JOURNAL	PATENT	WO 03004526-A	2005	16-JAN-2003
FEATURES	Molecular Engines Laboratories (FR)			
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US-09-966-880A-8	(1-198) x AX6733640	(1-17)		
QY	118 AspArgLysAlaGlu	122		
Db	1 GATCGCAAGGCTGAG	15		
RESULT 78				
AX673997/c				
LOCUS	AX673997	17 bp	DNA	linear
DEFINITION	Sequence 2442 from Patent WO03004526.			
ACCESSION	AX673997			
VERSION	AX673997.1	GI:29332345		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent: WO 03004526-A 1699 16-JAN-2003;			
FEATURES	Molecular Engines Laboratories (FR)			
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QY	59 LeuLeuPheLeuArg	63		
Db	17 CTTCTGTTTTCAGA	3		
RESULT 79				
AX674498				
LOCUS	AX674498	17 bp	DNA	linear
DEFINITION	Sequence 2943 from Patent WO03004526.			
ACCESSION	AX674498			
VERSION	AX674498.1	GI:29332846		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent: WO 03004526-A 1699 16-JAN-2003;			
FEATURES	Molecular Engines Laboratories (FR)			
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US-09-966-880A-8	(1-198) x AX673244	(1-17)		
QY	169 SerValArgLeuSer	173		
Db	3 TCCGTCGCGCTCAG	17		
RESULT 77				
AX673640				
LOCUS	AX673640	17 bp	DNA	linear
DEFINITION	Sequence 2085 from Patent WO03004526.			
ACCESSION	AX673640			
VERSION	AX673640.1	GI:29331988		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
JOURNAL	Patent: WO 03004526-A 1699 16-JAN-2003;			
FEATURES	Molecular Engines Laboratories (FR)			
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US-09-966-880A-8	(1-198) x AX673244	(1-17)		
QY	169 SerValArgLeuSer	173		
Db	3 TCCGTCGCGCTCAG	17		
RESULT 77				
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REFERENCE
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AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or resistance to viruses and their use as
  medicines
JOURNAL
  Patent: WO 03004526-A 2943 16-JAN-2003;
  Molecular Engines Laboratories (FR)
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
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Qy 169 SerValargLeuSer 173
Db 3 TCTGTCGCGCTCAGC 17
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AX723243
LOCUS AX723243 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 930 from Patent WO03025176.
ACCESSION AX723243
VERSION AX723243.1 GI:30423744
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
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JOURNAL
  Patent: WO 03025176-A 930 27-MAR-2003;
  Molecular Engines Laboratories (FR)
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Score: 5.00 Matches: 5
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
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Qy 71 AspProclargCys 75
Db 1 GATCCAGGCAGGTGT 15
RESULT 81
AX723989
LOCUS AX723989 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1676 from Patent WO03025176.
ACCESSION AX723989
VERSION AX723989.1 GI:30503332

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KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
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AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
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JOURNAL
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AX723989 (1-17)
Qy 179 IleLeuLeuProLeu 183
Db 2 ATCCTCTGGCACTG 16
RESULT 82
AX724877
LOCUS AX724877 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2564 from Patent WO03025176.
ACCESSION AX724877
VERSION AX724877.1 GI:30504220
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
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JOURNAL
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  Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX724877 (1-17)
Qy 43 SerLeuAspPheGly 47
Db 3 TCCCTGGACTTTGCT 17
RESULT 83

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AX726734
LOCUS       AX726734               17 bp    DNA
DEFINITION   Sequence 4421 from Patent WO03025176.
ACCESSION   AX726734
VERSION     AX726734.1 GI:30506077
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
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JOURNAL     Patent: WO 03025176-A 4421 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x AX726734 (1-17)

Qy
Db
2 ATCCTCTTCCCTCTC 16

RESULT 84
AX727644
LOCUS       AX727644               17 bp    DNA
DEFINITION   Sequence 5331 from Patent WO03025176.
ACCESSION   AX727644
VERSION     AX727644.1 GI:30506987
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 5331 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x AX727644 (1-17)

Qy
Db
2 ATCCTCTTCCCTCTC 16

RESULT 85
AX727871
LOCUS       AX727871               17 bp    DNA
DEFINITION   Sequence 5558 from Patent WO03025176.
ACCESSION   AX727871
VERSION     AX727871.1 GI:30507214
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
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JOURNAL     Patent: WO 03025176-A 5558 27-MAR-2003;
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US-09-966-880A-8 (1-198) x AX727871 (1-17)

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Db
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RESULT 86
AX728573
LOCUS       AX728573               17 bp    DNA
DEFINITION   Sequence 207 from Patent WO03025175.
ACCESSION   AX728573
VERSION     AX728573.1 GI:30507916
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
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JOURNAL     Patent: WO 03025175-A 207 27-MAR-2003;
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Qy
Db
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RESULT 85
AX727871
LOCUS       AX727871               17 bp    DNA
DEFINITION   Sequence 5558 from Patent WO03025176.
ACCESSION   AX727871
VERSION     AX727871.1 GI:30507214
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
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JOURNAL     Patent: WO 03025176-A 5558 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x AX727871 (1-17)

Qy
Db
2 ATCCTCTTCCCTCTC 16

RESULT 86
AX728573
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DEFINITION   Sequence 207 from Patent WO03025175.
ACCESSION   AX728573
VERSION     AX728573.1 GI:30507916
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
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JOURNAL     Patent: WO 03025175-A 207 27-MAR-2003;
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Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AX728573 (1-17)

Qy 83 SerTSPSerProCys 87
Db 3 TCCTGGAGCCCTGT 17

RESULT 87
LOCUS AX730844/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2478 from Patent WO03025175.
ACCESSION AX730844
VERSION AX730844.1 GI:30510187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2478 27-MAR-2003;
Molecular Engines Laboratories (FR)
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/organism="Homo sapiens"
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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX730844 (1-17)

Qy 132 AlaGlyValGlnIle 136
Db 15 GCTGGAGTGCAGATC 1

RESULT 88
LOCUS AX731908 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3542 from Patent WO03025175.
ACCESSION AX731908
VERSION AX731908.1 GI:30511251
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3542 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Score: 5.00 Matches: 5
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Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX731908 (1-17)

Qy 118 AspArgLysAlaGlu 122
Db 1 GATCGCAAGGCTGAG 15

RESULT 89
LOCUS AX735213 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 803 from Patent WO03025177.
ACCESSION AX735213
VERSION AX735213.1 GI:30514490
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 803 27-MAR-2003;
Molecular Engines Laboratories (FR)
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ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX735213 (1-17)

Qy 43 SerLeuAspPheGly 47
Db 3 TCTCTAGATTTCGT 17

RESULT 90
LOCUS AX735306 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 896 from Patent WO03025177.
ACCESSION AX735306
VERSION AX735306.1 GI:30514583
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 896 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers

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JOURNAL	thereof as medicaments
PATENT:	WO 03025177-A 1385 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR)
SOURCE	Location/Qualifiers
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ORIGIN	
Alignment Scores:	
Pred. No.:	7.93e+03
Score:	Length: 17
Percent Similarity:	Matches: 5
Best Local Similarity:	Conservative: 0
Query Match:	Mismatches: 0
DB:	Indels: 0
	Gaps: 0
US-09-966-880A-8 (1-198) x AX735795 (1-17)	
QY	59 LeuLeuPheLeuArg 63
Db	-----    17 CTCTTTTCTGAGA 3
RESULT 93	
AX739569	
LOCUS	AX739569 linear PAT 08-MAY-2003
DEFINITION	Sequence 5159 from Patent WO03025177.
ACCESSION	AX739569
VERSION	AX739569.1 GI:30518866
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE	1
	Teleman,A., Anson,R. and Tuijnder,M.
	Sequences involved in phenomena of tumour suppression, tumour
	reversion, apoptosis and/or resistance to viruses and the use
	thereof as medicaments
JOURNAL	Patent: WO 03025177-A 5159 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR)
SOURCE	Location/Qualifiers
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	/db_xref="taxon:9606"
ORIGIN	
Alignment Scores:	
Pred. No.:	7.93e+03
Score:	Length: 17
Percent Similarity:	Matches: 5
Best Local Similarity:	Conservative: 0
Query Match:	Mismatches: 0
DB:	Indels: 0
	Gaps: 0
US-09-966-880A-8 (1-198) x AX739569 (1-17)	
QY	118 AspArgLysalaGlu 122
Db	-----    1 GATCGCAAGGCTGAG 15
RESULT 94	
AX756969/c	
LOCUS	AX756969 linear PAT 25-JUN-2003
DEFINITION	Sequence 290 from Patent WO03040369.
ACCESSION	AX756969
VERSION	AX756969.1 GI:32251523
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 290 15-MAY-2003;
  Molecular Engines Laboratories (FR)
FEATURES
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Pred. No.:             5.00           Matches:      5
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:          2.53%          Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AX756969 (1-17)
Qy
46 PheGlyTyrLeuArg 50
Db
17 TTGGATATCTCAGA 3
RESULT 95
AX759927
LOCUS
  AX759927
DEFINITION
  Sequence 3248 from Patent WO03040369.
ACCESSION
  AX759927
VERSION
  AX759927.1 GI:32254543
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 3248 15-MAY-2003;
  Molecular Engines Laboratories (FR)
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Pred. No.:             5.00           Matches:      5
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:          2.53%          Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AX759927 (1-17)
Qy
179 IleLeuLeuProLeu 183
Db
2 ATCTCTGCTGCTCTG 16
RESULT 96
AX760197
LOCUS
  AX760197
DEFINITION
  Sequence 3518 from Patent WO03040369.
ACCESSION
  AX760197

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VERSION
  AX760197.1 GI:32254813
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 3518 15-MAY-2003;
  Molecular Engines Laboratories (FR)
FEATURES
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    /db_xref="taxon:9606"
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Alignment Scores:      7.93e+03      Length:      17
Pred. No.:             5.00           Matches:      5
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:          2.53%          Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AX760197 (1-17)
Qy
118 AspArgLysAlaGlu 122
Db
1 GATCGCAAGGCTCAG 15
RESULT 97
AX760666
LOCUS
  AX760666
DEFINITION
  Sequence 3987 from Patent WO03040369.
ACCESSION
  AX760666
VERSION
  AX760666.1 GI:32255282
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 3987 15-MAY-2003;
  Molecular Engines Laboratories (FR)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
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Alignment Scores:      7.93e+03      Length:      17
Pred. No.:             5.00           Matches:      5
Score:                 100.00%        Conservative: 0
Percent Similarity:    100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:          2.53%          Gaps:         0
DB:
US-09-966-880A-8 (1-198) x AX760666 (1-17)
Qy
179 IleLeuLeuProLeu 183
Db
2 ATCTGTTCCTCATG 16

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RESULT 98
AX762288
LOCUS AX762288 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5609 from Patent WO03040369.
ACCESSION AX762288
VERSION AX762288.1 GI:32256904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5609 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 7.93e+03 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AX762288 (1-17)

QY 118 AspArgLysAlaGlu 122
DB 1 GATCGCAAGCGCTGAG 15

RESULT 99
AX762491
LOCUS AX762491 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5812 from Patent WO03040369.
ACCESSION AX762491
VERSION AX762491.1 GI:32257107
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5812 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers
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/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 17 Length: 17
Score: 7.93e+03 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AX762491 (1-17)

QY 43 SerLeuLaspPheGly 47
DB 3 TCCTTAGATTGGG 17

RESULT 100
AX781934
LOCUS AX781934 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 265 from Patent WO03050284.
ACCESSION AX781934
VERSION AX781934.1 GI:32949768
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 265 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 7.93e+03 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AX781934 (1-17)

QY 3 SerLeuLeuMetAen 7
DB 3 AGTTTATTGATGAAT 17

RESULT 101
AX781935
LOCUS AX781935 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 266 from Patent WO03050284.
ACCESSION AX781935
VERSION AX781935.1 GI:32949769
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 266 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 7.93e+03 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AX781935 (1-17)

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US-09-966-880A-8 (1-198) x AX781935 (1-17)

Qy 3 SerLeuLeuMetAsn 7  
|||||  
Db 2 AGTTTATTGATGAAT 16

RESULT 102

AX781936 AX781936 17 bp DNA linear PAT 17-JUL-2003  
LOCUS Sequence 267 from Patent WO03050284.  
ACCESSION AX781936  
VERSION AX781936.1 GI:32949770  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
Guo,J.  
TITLE Human prostate cancer candidate protein 1  
JOURNAL Patent: WO 03050284-A 267 19-JUN-2003;  
Amersham Biosciences (SV) Corp. (US)

FEATURES  
source

1. .17  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores: 17  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX781936 (1-17)

Qy 3 SerLeuLeuMetAsn 7  
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Db 1 AGTTTATTGATGAAT 15

RESULT 103

BD105002/c BD105002 17 bp DNA linear PAT 27-AUG-2002  
LOCUS Kit and method for determining HLA type.  
DEFINITION  
ACCESSION BD105002  
VERSION BD105002.1 GI:22650576  
KEYWORDS WO 0192572-A/1106.  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE  
1 (bases 1 to 17)  
Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and  
Nishida,M.  
TITLE Kit and method for determining HLA type  
JOURNAL Patent: WO 0192572-A 1106 06-DEC-2001;  
NISHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO  
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO  
NISHIDA

COMMENT  
OS Artificial Sequence  
PN WO 0192572-A/1106  
PD 06-DEC-2001  
PF 01-JUN-2001 WO 2001JP004662  
PR 01-JUN-2000 JP 00P 164798  
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI  
MATSUMURA,  
SHOGO MORIYA, MICHIO NISHIDA  
CC C12Q1/68, C12M1/00, C12N15/09, G01N33/53  
PC Description of Artificial Sequence: capture  
FH Key Location/Qualifiers  
FT source 1. .17

FT Location/Qualifiers  
source

1. .17  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"

ORIGIN

Alignment Scores: 17  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD105002 (1-17)

Qy 112 ArgLeuTyrPheCys 116  
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Db 15 CGCTTGACTTCTGT 1

RESULT 104

BD200916 BD200916 17 bp RNA linear PAT 17-JUL-2003  
LOCUS Method and reagent for treating diseases or conditions concerning  
DEFINITION molecule participating in vasculogenic response.  
ACCESSION BD200916  
VERSION BD200916.1 GI:33010686  
KEYWORDS JP 2002509721-A/3942.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 17)  
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.  
TITLE Method and reagent for treating diseases or conditions concerning  
JOURNAL molecule participating in vasculogenic response  
COMMENT Patent: JP 2002509721-A 3942 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PN JP 2002509721-A/3942  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PI JAMES A MCSWIGGEN  
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00,  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00, A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
FH Key Location/Qualifiers  
FT source 1. .17  
/organism="Homo sapiens (human)"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:9606"

FEATURES  
source

1. .17  
Location/Qualifiers  
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/mol\_type="genomic RNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores: 17  
Pred. No.: 7.93e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

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US-09-966-880A-8 (1-198) x BD200916 (1-17)
Qy 177 ArgArgIleLeu 181
Db 1 AGAAGGATATGCTT 15

RESULT 105
A06176/c
LOCUS A06176 18 bp DNA linear PAT 04-JUN-1993
DEFINITION Oligonucleotide probe (reverse complement).
ACCESSION A06176
VERSION A06176.1 GI:411212
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE GENE MODIFICATION
JOURNAL Patent: WO 9001549-A 4 22-FEB-1990;
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A06176 (1-18)
Qy 35 ArgArgAspSerAla 39
Db 17 CGCCGTCAGCTCAGCA 3

RESULT 106
A40057/c
LOCUS A40057 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 18 from Patent WO9421818.
ACCESSION A40057
VERSION A40057.1 GI:2296222
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Andrien,M., Dupont,E., Rossau,R. and De,C.I.
TITLE PROCESS FOR TYPING HLA-B USING SPECIFIC PRIMERS AND PROBES SETS
JOURNAL INNOCENTICS NV (BE)
COMMENT Patent: WO 9421818-A 18 29-SEP-1994;
Other publication CA 2158578 940929
Other publication AU 6258594 941011.
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A40057 (1-18)
Qy 112 ArgLeuTyrPheCys 116
Db 17 CGCTTGACTTCGT 3

RESULT 107
AR016419
LOCUS AR016419 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776725.
ACCESSION AR016419
VERSION AR016419.1 GI:3972696
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kindsvogel,W.R., Jelinek,L.J., Sheppard,P.O., Grant,F.J.,
Kuijper,J.L., Foster,D.C., Lok,S. and O'Hara,P.J.
TITLE Recombinant production of glucagon receptors
JOURNAL Patent: US 5776725-A 2 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR016419 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 108
AR072241
LOCUS AR072241 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 44 from patent US 5948611.
ACCESSION AR072241
VERSION AR072241.1 GI:99999005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvanemi,P.,
Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
TITLE Primers and methods for detecting mutations in the procollagen II
gene (COL2A1) that indicate a genetic predisposition for a
COL2AI-associated disease
JOURNAL Patent: US 5948611-A 44 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR072241 (1-18)

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QY 69 AspLeuAspProGly 73
Db 3 GATCTGGATCCTGGA 17

RESULT 109
LOCUS AR073074/c 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 47 from patent US 5948680..
ACCESSION AR073074
VERSION AR073074.1 GI:9999837
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker, B.F. and Cowseert, L.M.
TITLE Antisense inhibition of Elk-1 expression
JOURNAL Patent: US 5948680-A 47 07-SEP-1999;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR073074 (1-18)

QY 103 AsnLeuSerLeuArg 107
Db 17 AACCTTTCTCTCAGA 3

RESULT 110
LOCUS AR076296 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 10 from patent US 5958771.
ACCESSION AR076296
VERSION AR076296.1 GI:10003042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C. Frank., Ackermann, E.J. and Cowseert, L.M.
TITLE Antisense modulation of cellular inhibitor of Apoptosis-2
expression
JOURNAL Patent: US 5958771-A 10 28-SEP-1999;
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR076296 (1-18)

QY 59 LeuLeuPheLeuArg 63
Db 4 CTTTATTCTTCTAGA 18

RESULT 111
LOCUS AR076328 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 42 from patent US 5958771.
ACCESSION AR076328
VERSION AR076328.1 GI:10003074
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C. Frank., Ackermann, E.J. and Cowseert, L.M.
TITLE Antisense modulation of cellular inhibitor of Apoptosis-2
expression
JOURNAL Patent: US 5958771-A 42 28-SEP-1999;
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR076328 (1-18)

QY 38 SerAlaThrSerPhe 42
Db 4 AGTCTACCTCTTTT 18

RESULT 112
LOCUS AR094003 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 19 from patent US 6001597.
ACCESSION AR094003
VERSION AR094003.1 GI:10020748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond, C.K. and Vanaja, E.
TITLE Compositions and methods for producing heterologous polypeptides in
Pichia methanolica
JOURNAL Patent: US 6001597-A 19 14-DEC-1999;
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR094003 (1-18)

QY 32 ValValIysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 113
LOCUS AR096629 36 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 36 from patent US 6001597.
ACCESSION AR096629
VERSION AR096629.1 GI:10020748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Raymond, C.K. and Vanaja, E.
TITLE Compositions and methods for producing heterologous polypeptides in
Pichia methanolica
JOURNAL Patent: US 6001597-A 36 14-DEC-1999;
FEATURES
    Location/Qualifiers
    source
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    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 36
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR096629 (1-36)

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```
LOCUS       AR096629               18 bp      DNA
DEFINITION   Sequence 13 from patent US 6008048.
ACCESSION    AR096629
VERSION      AR096629.1  GI:10025595
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Monia,B.P. and Cowsext,L.M.
TITLE        Antisense inhibition of EGR-1 expression
JOURNAL      Patent: US 6008048-A 13 28-DEC-1999;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6             Gaps:          0
US-09-966-880A-8 (1-198) x AR096629 (1-18)
QY          127 ArgArgLeuHisArg 131
Db          4 CGCGCGCTCCACGC 18
RESULT 114
LOCUS       AR098797/c             18 bp      DNA
DEFINITION   Sequence 52 from patent US 6077672.
ACCESSION    AR098797
VERSION      AR098797.1  GI:12808563
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Monia,B.P. and Cowsext,L.M.
TITLE        Antisense modulation of TRADD expression
JOURNAL      Patent: US 6077672-A 52 20-JUN-2000;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6             Gaps:          0
US-09-966-880A-8 (1-198) x AR098797 (1-18)
QY          121 AlaGluProGluGly 125
Db          16 GCTGAGCTCGAAGGA 2
RESULT 115
LOCUS       AR119891             18 bp      DNA
DEFINITION   Sequence 19 from patent US 6153424.
ACCESSION    AR119891
VERSION      AR119891.1  GI:14102590
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Raymond,C.K.
TITLE        Protease-deficient strains of Pichia methanolica
JOURNAL      Patent: US 6153424-A 19 28-NOV-2000;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6             Gaps:          0
US-09-966-880A-8 (1-198) x AR119891 (1-18)
QY          32 ValValIysArgArg 36
Db          2 GTTGTAACGACGG 16
RESULT 116
LOCUS       AR124397             18 bp      DNA
DEFINITION   Sequence 172 from patent US 6171859.
ACCESSION    AR124397
VERSION      AR124397.1  GI:14109758
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Herrnstadt,C. and Parker,W.Davis.
TITLE        Method of targeting conjugate molecules to mitochondria
JOURNAL      Patent: US 6171859-A 172 09-JAN-2001;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6             Gaps:          0
US-09-966-880A-8 (1-198) x AR124397 (1-18)
QY          125 GlyLeuArgArgLeu 129
Db          2 GGTCTACGAGGAGCTC 16
RESULT 117
LOCUS       AR128108             18 bp      DNA
DEFINITION   Sequence 17 from patent US 6183953.
ACCESSION    AR128108
VERSION      AR128108.1  GI:14115770
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Raymond,C.K.
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TITLE Chromosomal mutagenesis in *Pichia methanolica*  
JOURNAL Patent: US 6183953-A 17 06-FEB-2001;  
FEATURES Location/Qualifiers

source

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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR128108 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 118

AR138197

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR138197 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

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/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

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ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

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/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallyysArgArg 36

apoptosis-2.

ACCESSION BD234560  
VERSION BD234560.1 GI:33044330  
KEYWORDS JP 2002531102-A/42.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Bennett,F.C., Ackermann,E.J. and Cowsett,L.M.  
TITLE Antisense modulation of expression of cellular inhibitor of  
JOURNAL Patent: JP 2002531102-A 42 24-SEP-2002;  
ISIS PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002531102-A/42  
PD 24-SEP-2002  
PF 23-SEP-1999 JP 2000585449  
PR 03-DEC-1998 US 09/205144  
PI FRANK C BENNETT,ELIZABETH J ACKERMANN,LEX M COWSETT PC  
C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K31/713,A61K48/PC  
00,  
CC A61P35/00,A61P37/00,C12N15/00  
PC Synthetic  
FH Key Location/Qualifiers  
FT source i.18  
FT /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x BD234560 (1-18)  
Cyt  
38 SerAlaThrSerPhe 42  
|||||  
4 AGTGCTACCTCTTT 18  
RESULT 122  
BD237570  
LOCUS  
DEFINITION Cytokine receptor ZALPHA11.  
ACCESSION BD237570  
VERSION BD237570.1 GI:33047340  
KEYWORDS JP 2002526062-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.  
TITLE Cytokine receptor ZALPHA11  
JOURNAL Patent: JP 2002526062-A 4 20-AUG-2002;  
ZMOGENETICS INC  
COMMENT OS Artificial Sequence  
PN JP 2002526062-A/4  
PD 20-AUG-2002  
PF 23-SEP-1999 JP 2000574143  
PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR  
06-JUL-1999 US 09/347930  
PI SCOTT R PRESNELL,DARRELL C CONKLIN,JULIA E NOVAK,ANGELA K PI  
HAMMOND  
PC C12N15/09,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21,PC  
C12N5/10,  
PC C12P21/08,C12Q1/02,G01N33/53,G01N33/566,C12N15/00,  
PC C12N5/00

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Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 124
BD244729/C
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Isolation method of primer extension products by modular
oligonucleotide.
ACCESSION BD244729.1 GI:33054499
VERSION BD244729
KEYWORDS JP 2002525076-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lundeberg, J. and Uhlen, M.
TITLE Isolation method of primer extension products by modular
JOURNAL Patent: JP 2002525076-A 8 13-AUG-2002;
DYNAL AS
COMMENT OS Artificial Sequence
PN JP 2002525076-A/8
PD 13-AUG-2002
PF 15-SEP-1998 JP 2000570369
PR 15-SEP-1998 US 09/153242.16-SEP-1998 GB 9820185.8 PI
PC C12N15/09,C12Q1/68,C12N15/00
CC JOAKIM LUNDEBERG, MATHIAS UHLEN
CC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: Synthetic oligonucleotide
FT pUC18/PRIT28, forward, modulating module, generic FH Key
FT Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
1..18 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x BD244729 (1-18)

Qy 32 ValVallysArgArg 36
Db 17 GTTGTAAACGACGG 3

RESULT 125
BD248283
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Polypeptide zsig58 of pancreas and ovary.
ACCESSION BD248283
VERSION BD248283.1 GI:33058053
KEYWORDS JP 2002524043-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shepard, P.O. and Chandrasekhar, Y.
TITLE Polypeptide zsig58 of pancreas and ovary
JOURNAL Patent: JP 2002524043-A 3 06-AUG-2002;
ZYMOGENETICS INC
COMMENT OS Artificial Sequence
PN JP 2002524043-A/3
PD 06-AUG-2002

PF 03-AUG-1999 JP 2000563779
PR 03-AUG-1998 US 09/128372
PI PAUL O SHEPPARD, YASMIN CHANDRASEKHAR
PC C12N15/09,C07K14/47,C07K16/46,C07K19/00,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02,G01N33/15, PC
G01N33/50//
PC (C12P21/02,C12R1:19), (C12P21/02,C12R1:91),C12N15/00,C12N5/00
CC Oligonucleotide primer: ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
1..18 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x BD248283 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 126
BD249010
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION BD249010
VERSION BD249010.1 GI:33058780
KEYWORDS JP 2002537839-A/71.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak, J.E., Presnell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D.,
Gross, J.A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and
Hammond, A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 71 12-NOV-2002;
ZYMOGENETICS INC
COMMENT OS Artificial Sequence
PN JP 2002537839-A/71
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
01-JUL-1999 US 60/142013
PI JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,
PI RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON,
PI STACEY R DILLON, ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
1..18 /organism='synthetic construct'

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Db 4 CTTTATTCTTAGA 18

RESULT 128  
BD250638

LOCUS  
DEFINITION  
BD250638 18 bp DNA linear PAT 17-JUL-2003  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation.

ACCESSION  
BD250638  
VERSION  
JP 2002511276-A/192.  
KEYWORDS  
GI:33060408  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Cowser, L.M., Baker, B.F., Mcneil, J., Freier, S.M., Sasnor, H.M., Brooks, D.G., Ohasi, C., Wyatt, J.R., Borchers, A.H. and Vikkars, T.A.  
TITLE  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation  
JOURNAL  
Patent: JP 2002511276-A 192 16-APR-2002;  
COMMENT  
ISIS PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002511276-A/192  
PD 16-APR-2002  
PF 13-APR-1999 JP 2000543647  
PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI  
LEX M COWSERT, BRENDA F BAKER, JOHN MCNEIL, SUSAN M FRIER, HENRI PI  
M SASMOR,  
PI DOUGLAS G BROOKS, CARA OHASI, JACQUELINE R WYATT, ALEXANDER H PI  
BORCHERS,  
PI TIMOTHY A VIKKARS  
PC C12N15/09, C07B61/00, C12Q1/68, G06F17/30, G06F17/50, PC  
C12N15/00  
CC Antisense Oligonucleotide  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence',  
/mol\_type='genomic DNA',  
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ORIGIN

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD250638 (1-18)

QY 38 SerAlaThrSerPhe 42  
|||||  
4 AGTGTACTCTTTT 18

Db

RESULT 129  
BD250687/c

LOCUS  
DEFINITION  
BD250687 18 bp DNA linear PAT 17-JUL-2003  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation.

ACCESSION  
BD250687  
VERSION  
JP 2002511276-A/241.  
KEYWORDS  
GI:33060457  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Cowser, L.M., Baker, B.F., Mcneil, J., Freier, S.M., Sasnor, H.M., Brooks, D.G., Ohasi, C., Wyatt, J.R., Borchers, A.H. and Vikkars, T.A.

QY 59 LeuLeuPheIeuArg 63  
|||||  
59 LeuLeuPheIeuArg 63

Db 4 CTTTATTCTTAGA 18

RESULT 128  
BD250638

LOCUS  
DEFINITION  
BD250638 18 bp DNA linear PAT 17-JUL-2003  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation.

ACCESSION  
BD250638  
VERSION  
JP 2002511276-A/192.  
KEYWORDS  
GI:33060408  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Cowser, L.M., Baker, B.F., Mcneil, J., Freier, S.M., Sasnor, H.M., Brooks, D.G., Ohasi, C., Wyatt, J.R., Borchers, A.H. and Vikkars, T.A.  
TITLE  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation  
JOURNAL  
Patent: JP 2002511276-A 192 16-APR-2002;  
COMMENT  
ISIS PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002511276-A/192  
PD 16-APR-2002  
PF 13-APR-1999 JP 2000543647  
PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI  
LEX M COWSERT, BRENDA F BAKER, JOHN MCNEIL, SUSAN M FRIER, HENRI PI  
M SASMOR,  
PI DOUGLAS G BROOKS, CARA OHASI, JACQUELINE R WYATT, ALEXANDER H PI  
BORCHERS,  
PI TIMOTHY A VIKKARS  
PC C12N15/09, C07B61/00, C07B61/00, C12Q1/68, G06F17/30, G06F17/50, PC  
C12N15/00  
CC Antisense Oligonucleotide  
FH Key Location/Qualifiers  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x BD250638 (1-18)

QY 38 SerAlaThrSerPhe 42  
|||||  
4 AGTGTACTCTTTT 18

Db

RESULT 129  
BD250687/c

LOCUS  
DEFINITION  
BD250687 18 bp DNA linear PAT 17-JUL-2003  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation.

ACCESSION  
BD250687  
VERSION  
JP 2002511276-A/241.  
KEYWORDS  
GI:33060457  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Cowser, L.M., Baker, B.F., Mcneil, J., Freier, S.M., Sasnor, H.M., Brooks, D.G., Ohasi, C., Wyatt, J.R., Borchers, A.H. and Vikkars, T.A.

ORIGIN  
Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x BD250606 (1-18)

QY 59 LeuLeuPheIeuArg 63  
|||||  
59 LeuLeuPheIeuArg 63

TITLE Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.  
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation

JOURNAL ISIS PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2002511276-A/241  
PD 16-APR-2002  
PF 13-APR-1999 JP 2000543647  
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI  
LEX M CONWERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI  
M SASMOR,  
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI  
BORCHERS,  
PI TIMOTHY A VIKKARS  
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC  
C12N15/00  
CC Identification of genetic targets for modulation by CC  
oligonucleotides and  
CC generation of oligonucleotides for gene modulation FH Key  
Location/Qualifiers  
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FT /Organism='Artificial Sequence'.  
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/db\_xref="taxon:32630"

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Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD250687 (1-18)

QY 103 AsnLeuSerLeuArg 107  
Db 17 AACCTTCTCTCAGA 3

RESULT 130  
BD251856  
LOCUS RING finger protein ZAP03. 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION  
ACCESSION BD251856  
VERSION BD251856.1 GI:33061626  
KEYWORDS JP 2002530061-A/10.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Venezia,D. and Grossmann,A.  
TITLE RING finger protein ZAP03  
JOURNAL Patent: JP 2002530061-A 10 17-SEP-2002;  
ZYMOMETICS INC  
COMMENT OS Artificial Sequence  
PN JP 2002530061-A/10  
PD 17-SEP-2002  
PF 04-NOV-1999 JP 2000582416  
PR 12-NOV-1998 US 09/191500  
PI DOMENICK VENEZIA, ANGELIKA GROSSMANN  
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
10,  
PC C12P21/02,C12Q1/02//C12P21/08,C12N15/00,C12N5/00 CC  
Oligonucleotide primer ZC976  
FH Key Location/Qualifiers  
FT source 1. .18

FEATURES  
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Location/Qualifiers  
1. .18  
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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD251856 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

RESULT 131  
BD272777  
LOCUS Adipocyte-specific protein homolog ZACRP3. 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION  
ACCESSION BD272777  
VERSION BD272777.1 GI:33082545  
KEYWORDS JP 2002541847-A/13.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Piddington,C.S. and Bishop,P.D.  
TITLE Adipocyte-specific protein homolog ZACRP3  
JOURNAL Patent: JP 2002541847-A 13 10-DEC-2002;  
ZYMOMETICS INC  
COMMENT OS Artificial Sequence  
PN JP 2002541847-A/13  
PD 10-DEC-2002  
PF 19-APR-2000 JP 2000612456  
PR 20-APR-1999 US 09/294943  
PI CHRISTOPHER S PIDDINGTON, PAUL D BISHOP  
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
10,  
PC C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/53,G01N33/577,  
PC C12N15/00,  
PC C12N5/00  
CC Oligonucleotide ZC976  
FH Key Location/Qualifiers  
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FT /Organism='Artificial Sequence'.  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
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ORIGIN

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Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD272777 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

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RESULT 132
LOCUS       126352
DEFINITION  Sequence 44 from patent US 5558988.
ACCESSION  126352
VERSION    126352.1
KEYWORDS   GI:1606222
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
TITLE      Primers and methods for detecting mutations in the procollagen II
FEATURES   Gene that indicate a genetic predisposition for osteoarthritis
JOURNAL    Patent: US 5558988-A 44 24-SEP-1996;
LOCUS       126352
DEFINITION  Sequence 1123 from patent US 5731295.
ACCESSION  126352
VERSION    126352.1
KEYWORDS   GI:3939430
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
           Stinchcomb,D.T.
TITLE      Method of reducing stromelysin RNA via ribozymes
JOURNAL    Patent: US 5731295-A 1123 24-MAR-1998;
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:       0
DB:             6            Gaps:        0
US-09-966-880A-8 (1-198) x I26352 (1-18)
QY          69 AspLeuAspProGly 73
DB          3 GATCTGGATCCTCGA 17
RESULT 133
LOCUS       138110/c
DEFINITION  Sequence 1123 from patent US 5612215.
ACCESSION  138110
VERSION    138110.1
KEYWORDS   GI:2086100
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
           Stinchcomb,D.T.
TITLE      Stromelysin targeted ribozymes
JOURNAL    Patent: US 5612215-A 1123 18-MAR-1997;
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
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Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:       0
DB:             6            Gaps:        0
US-09-966-880A-8 (1-198) x I38110 (1-18)
QY          119 ArgLysAlaGluPro 123
DB          15 AGAAGGCGGACCG 1
RESULT 134
LOCUS       194960
DEFINITION  Sequence 1123 from patent US 5731295.
ACCESSION  194960
VERSION    194960.1
KEYWORDS   GI:3939430
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
           Stinchcomb,D.T.
TITLE      Method of reducing stromelysin RNA via ribozymes
JOURNAL    Patent: US 5731295-A 1123 24-MAR-1998;
FEATURES   Location/Qualifiers
            source
            1..18
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            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:       0
DB:             6            Gaps:        0
US-09-966-880A-8 (1-198) x I94960 (1-18)
QY          119 ArgLysAlaGluPro 123
DB          15 AGAAGGCGGACCG 1
RESULT 135
LOCUS       AR194048
DEFINITION  Sequence 20 from patent US 6348331.
ACCESSION  AR194048
VERSION    AR194048.1
KEYWORDS   GI:20240640
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Raymond,C.K.
TITLE      Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 2
JOURNAL    Patent: US 6348331-A 20 19-FEB-2002;
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:       0
DB:             6            Gaps:        0
US-09-966-880A-8 (1-198) x AR194048 (1-18)
QY          32 ValVallysArgArg 36
DB          2 GTTGTAAACGACGG 16
RESULT 136
LOCUS       AR207354
DEFINITION  Sequence 10 from patent US 6372889.
ACCESSION  AR207354

```

```
VERSION AR207354.1 GI:21506241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O., Conklin,D.C., Farrah,T.M., Maurer,M.F. and Grossmann,A.
TITLE Soluble protein ZTMPO-1
JOURNAL Patent: US 6372889-A 10 16-APR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AR207354 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 137
LOCUS AR224080 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 12 from patent US 6440697.
ACCESSION AR224080
VERSION AR224080.1 GI:23332738
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Venezia,D. and Grossmann,A.
TITLE Ring finger protein zap03
JOURNAL Patent: US 6440697-A 12 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AR224080 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 138
LOCUS AR224401 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6440720.
ACCESSION AR224401
VERSION AR224401.1 GI:23333178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using
```

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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K.
TITLE Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 2
JOURNAL Patent: US 640720-A 20 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AR224401 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 139
LOCUS AR243306/c 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6475781.
ACCESSION AR243306
VERSION AR243306.1 GI:27290496
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mercola,M.K., Deininger,P.L. and Stiles,C.D.
TITLE Trans-dominant suppressor genes for oligomeric proteins
JOURNAL Patent: US 6475781-A 7 05-NOV-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AR243306 (1-18)
Qy 59 LeuLeuPheLeuArg 63
Db 17 CTTCCTTCCTGCGA 3
RESULT 140
LOCUS AR255248/c 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6482592.
ACCESSION AR255248
VERSION AR255248.1 GI:27304297
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
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JOURNAL  
Patent: US 6482592-A 8 19-NOV-2002;  
FEATURES  
Location/Qualifiers  
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## ORIGIN

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Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR255248 (1-18)

Qy 32 ValVallysArgArg 36  
|||||  
Db 17 GTTGTAACGACGG 3

## RESULT 141

LOCUS AR255758 18 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 12 from patent US 6482612.  
ACCESSION AR255758  
VERSION AR255758.1 GI:27304877  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Shepard,P.O. and Humes,J.M.  
TITLE Adipocyte-specific protein homologs  
JOURNAL Adipocyte Complement Related Protein Homolog zacr3  
FEATURES  
Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR255758 (1-18)

Qy 32 ValVallysArgArg 36  
|||||  
Db 2 GTTGTAACGACGG 16

## RESULT 142

LOCUS AR281831 18 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 19 from patent US 6521233.  
ACCESSION AR281831  
VERSION AR281831.1 GI:29717673  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Piddington,C.S. and Bishop,P.D.  
TITLE Adipocyte complement related protein homolog zacr3  
JOURNAL Adipocyte Complement Related Protein Homolog zacr3  
FEATURES  
Location/Qualifiers  
source  
1. .18  
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## ORIGIN /mol\_type="genomic DNA"

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR281831 (1-18)

Qy 32 ValVallysArgArg 36  
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Db 2 GTTGTAACGACGG 16

## RESULT 143

LOCUS AR294884 18 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 6619 from patent US 6537751.  
ACCESSION AR294884  
VERSION AR294884.1 GI:31682168  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
JOURNAL disequilibrium map of the human genome  
FEATURES  
Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR294884 (1-18)

Qy 102 ProAnLeuSerLeu 106  
|||||  
Db 4 CCAATCTATCCCTC 18

## RESULT 144

LOCUS AR298608 18 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 10343 from patent US 6537751.  
ACCESSION AR298608  
VERSION AR298608.1 GI:31685892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
JOURNAL disequilibrium map of the human genome  
FEATURES  
Location/Qualifiers  
source  
1. .18  
/organism="unknown"  
/mol\_type="genomic DNA"



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Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:         0
DB:             6            Gaps:           0

US-09-966-880A-8 (1-198) x AR298608 (1-18)

QY 34 LysArgArgAspSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 145
LOCUS AR342878 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6576744.
ACCESSION AR342878
VERSION AR342878.1 GI:33738177
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL
FEATURES
    source
    Location/Qualifiers
    1..18
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    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
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Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:         0
DB:             6            Gaps:           0

US-09-966-880A-8 (1-198) x AR342878 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 146
LOCUS AR364357 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 10 from patent US 5262866.
ACCESSION AR364357
VERSION AR364357.1 GI:34426820
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Hong,S.-H.
TITLE Method for displaying a plurality of sequential video images in a
JOURNAL multi-screen picture
FEATURES
    source
    Location/Qualifiers
    1..18
    /organism="unknown"
    /mol_type="genomic DNA"
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Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Query Match:    2.53%         Indels:         0
DB:             6            Gaps:           0

US-09-966-880A-8 (1-198) x AR364357 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 147
LOCUS AR374109 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 77 from patent US 6605272.
ACCESSION AR374109
VERSION AR374109.1 GI:40076681
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 77 12-AUG-2003;
FEATURES
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    Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:         0
DB:             6            Gaps:           0

US-09-966-880A-8 (1-198) x AR374109 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 148
LOCUS AR392008 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6613547.
ACCESSION AR392008
VERSION AR392008.1 GI:40115784
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K., Vanaja,E., Miller,B.G. and Sloan,J.S.
TITLE Pichia methanolica glyceraldhyde-3-phosphate dehydrogenase 1
JOURNAL promoter and terminator
FEATURES
    source
    Location/Qualifiers
    1..18
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    /mol_type="genomic DNA"
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Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:         0
DB:             6            Gaps:           0

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DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR392008 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 149
AR399695
LOCUS AR399695 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 19 from patent US 6620909.
ACCESSION AR399695
VERSION AR399695.1 GI:40142170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp2
JOURNAL Patent: US 6620909-A 19 16-SEP-2003;
FEATURES
    Location/Qualifiers
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                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR399695 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 150
AR399963
LOCUS AR399963 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 19 from Patent WO0063377.
ACCESSION AR399963
VERSION AR399963.1 GI:11229983
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp3
JOURNAL Patent: WO 0063377-A 19 26-OCT-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
        source
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ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX039963 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 151
AR399983
LOCUS AR399983 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 19 from Patent WO0063376.
ACCESSION AR399983
VERSION AR399983.1 GI:11229998
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp2
JOURNAL Patent: WO 0063376-A 19 26-OCT-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide ZC976"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX039983 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 152
AR055856
LOCUS AR055856 18 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 28 from Patent WO0073459.
ACCESSION AR055856
VERSION AR055856.1 GI:12228964
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S., West,J.R., Holly,R.D. and Burkhead,S.K.
TITLE Four-helical bundle protein zsig81
JOURNAL Patent: WO 0073459-A 28 07-DEC-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

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US-09-966-880A-8 (1-198) x AX055856 (1-18)

QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16

## RESULT 153

LOCUS AX061885 18 bp DNA linear PAT 24-JAN-2001  
DEFINITION Sequence 18 from Patent WO0078978.  
ACCESSION AX061885

VERSION AX061885.1 GI:12539931  
KEYWORDS synthetic construct

SOURCE synthetic construct  
ORGANISM artificial sequences.

## REFERENCE

1 Miller,B.G., Sloan,J.S., Raymond,C.K. and Vanaaja,E.

Pichia methanolica glyceralddehyde-3-phosphate dehydrogenase 1

AUTHORS promoter and terminator

TITLE Patent: WO 0078978-A 18 28-DEC-2000;

JOURNAL ZymoGenetics, Inc. (US) ; Miller, Brady G. (US) ; Sloan, James S.

(US)

FEATURES Location/Qualifiers

source  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer ZC976"

## ORIGIN

Alignment Scores: 8.33e+03 Length: 18  
Pred. No.: 5  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX061885 (1-18)

QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16

## RESULT 154

LOCUS AX093416 18 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 20 from Patent WO0118182.  
ACCESSION AX093416

VERSION AX093416.1 GI:13509866  
KEYWORDS synthetic construct

SOURCE synthetic construct  
ORGANISM artificial sequences.

## REFERENCE

1 Raymond,C.K.

Pichia methanolica glyceralddehyde-3-phosphate dehydrogenase 2

AUTHORS promoter and terminator

TITLE Patent: WO 0118182-A 20 15-MAR-2001;

JOURNAL ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

source  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer ZC976"

## ORIGIN

Alignment Scores: 8.33e+03 Length: 18  
Pred. No.: 5  
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX093416 (1-18)

QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16

## RESULT 155

LOCUS AX172752 18 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 8 from Patent WO0142292.  
ACCESSION AX172752

VERSION AX172752.1 GI:14597848  
KEYWORDS synthetic construct

SOURCE synthetic construct  
ORGANISM artificial sequences.

## REFERENCE

1 Sheppard,P.O.

Secreted polypeptide zsig87

TITLE Patent: WO 0142292-A 8 14-JUN-2001;

JOURNAL ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

source  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer ZC976"

## ORIGIN

Alignment Scores: 8.33e+03 Length: 18  
Pred. No.: 5  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX172752 (1-18)

QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16

## RESULT 156

LOCUS AX179621 18 bp DNA linear PAT 06-AUG-2001  
DEFINITION Sequence 44 from Patent WO0146422.  
ACCESSION AX179621

VERSION AX179621.1 GI:15132047  
KEYWORDS synthetic construct

SOURCE synthetic construct  
ORGANISM artificial sequences.

## REFERENCE

1 Presnell,S.R. and Kindsvogel,W.

Cytokine zcyto18

TITLE Patent: WO 0146422-A 44 28-JUN-2001;

JOURNAL ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

source  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer ZC976"

## ORIGIN

Alignment Scores: 8.33e+03 Length: 18  
Pred. No.: 5  
Score: 5.00 Matches: 5

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX179621 (1-18)

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 157

AX233363 AX233363 18 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 6 from Patent WO0162788.

DEFINITION AX233363

ACCESSION AX233363

VERSION AX233363.1 GI:15592697

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.

TITLE Corneodesmosin based test and model for inflammatory disease

JOURNAL Patent: WO 0162788-A 6 30-AUG-2001;

OXAGEN Limited (GB)

FEATURES Location/Qualifiers

1..18

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

ORIGIN

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233363 (1-18)

Qy 129 LeuHisArgAlaGly 133  
Db 3 CTCACAGAGCTGGA 17

RESULT 158

AX233461 AX233461 18 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 104 from Patent WO0162788.

DEFINITION AX233461

ACCESSION AX233461

VERSION AX233461.1 GI:15592892

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.

TITLE Corneodesmosin based test and model for inflammatory disease

JOURNAL Patent: WO 0162788-A 104 30-AUG-2001;

OXAGEN Limited (GB)

FEATURES Location/Qualifiers

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/db\_xref="taxon:32630"

/note="primer"

ORIGIN

Alignment Scores:

Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233461 (1-18)

Qy 129 LeuHisArgAlaGly 133  
Db 3 CTCACAGAGCTGGA 17

RESULT 159

AX233463 AX233463 18 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 106 from Patent WO0162788.

DEFINITION AX233463

ACCESSION AX233463

VERSION AX233463.1 GI:15592898

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.

TITLE Corneodesmosin based test and model for inflammatory disease

JOURNAL Patent: WO 0162788-A 106 30-AUG-2001;

OXAGEN Limited (GB)

FEATURES Location/Qualifiers

1..18

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

ORIGIN

Alignment Scores:  
Pred. No.: 8.33e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233463 (1-18)

Qy 129 LeuHisArgAlaGly 133  
Db 3 CTCACAGAGCTGGA 17

RESULT 160

AX233464 AX233464 18 bp DNA linear PAT 11-SEP-2001  
LOCUS Sequence 107 from Patent WO0162788.

DEFINITION AX233464

ACCESSION AX233464

VERSION AX233464.1 GI:15592901

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.

TITLE Corneodesmosin based test and model for inflammatory disease

JOURNAL Patent: WO 0162788-A 107 30-AUG-2001;

OXAGEN Limited (GB)

FEATURES Location/Qualifiers

1..18

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

ORIGIN

Alignment Scores:

ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
US-09-966-880A-8 (1-198) x AX713216 (1-18)			8.33e+03	5.00	100.00%	2.53%	6	18 bp	5	0	0	0	0
QY	129	LeuHisArgAlaGly	133										
Db	3	CTCCACAGAGCTGGA	17										
RESULT 161													
LOCUS	AX548073												
DEFINITION	Sequence 22 from Patent WO234917.												
ACCESSION	AX548073												
VERSION	AX548073.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Conklin,D.C., Gao,Z., Lofton-Day,C.E. and Whitmore,T.E.												
TITLE	Secreted alpha-helical protein zlm2a24												
JOURNAL	Patent: WO 0234917-A 22 02-MAY-2002;												
FEATURES	ZymoGenetics, Inc. (US)												
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ORIGIN													
Alignment Scores:													
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Score:			5.00										
Percent Similarity:			100.00%										
Best Local Similarity:			100.00%										
Query Match:			2.53%										
DB:			6										
US-09-966-880A-8 (1-198) x AX548073 (1-18)													
QY	32	ValValLysArgArg	36										
Db	2	GTGTAAACGACGG	16										
RESULT 162													
LOCUS	AX713216/c												
DEFINITION	Sequence 102 from Patent WO03018837.												
ACCESSION	AX713216												
VERSION	AX713216.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Waschuetza,S., Schnakenberg,E. and Lustig,M.												
TITLE	Method and diagnostic kit for the molecular diagnosis of												

ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
US-09-966-880A-8 (1-198) x AX713216 (1-18)			8.33e+03	5.00	100.00%	2.53%	6	18 bp	5	0	0	0	0
QY	129	LeuHisArgAlaGly	133										
Db	3	CTCCACAGAGCTGGA	17										
RESULT 161													
LOCUS	AX548073												
DEFINITION	Sequence 22 from Patent WO234917.												
ACCESSION	AX548073												
VERSION	AX548073.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Conklin,D.C., Gao,Z., Lofton-Day,C.E. and Whitmore,T.E.												
TITLE	Secreted alpha-helical protein zlm2a24												
JOURNAL	Patent: WO 0234917-A 22 02-MAY-2002;												
FEATURES	ZymoGenetics, Inc. (US)												
source	Location/Qualifiers												
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ORIGIN													
Alignment Scores:													
Pred. No.:			8.33e+03	5.00	100.00%	2.53%	6	18 bp	5	0	0	0	0
Score:			5.00										
Percent Similarity:			100.00%										
Best Local Similarity:			100.00%										
Query Match:			2.53%										
DB:			6										
US-09-966-880A-8 (1-198) x AX548073 (1-18)													
QY	32	ValValLysArgArg	36										
Db	2	GTGTAAACGACGG	16										
RESULT 162													
LOCUS	AX713216/c												
DEFINITION	Sequence 102 from Patent WO03018837.												
ACCESSION	AX713216												
VERSION	AX713216.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Waschuetza,S., Schnakenberg,E. and Lustig,M.												
TITLE	Method and diagnostic kit for the molecular diagnosis of												

ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
US-09-966-880A-8 (1-198) x AX713216 (1-18)			8.33e+03	5.00	100.00%	2.53%	6	18 bp	5	0	0	0	0
QY	129	LeuHisArgAlaGly	133										
Db	3	CTCCACAGAGCTGGA	17										
RESULT 161													
LOCUS	AX548073												
DEFINITION	Sequence 22 from Patent WO234917.												
ACCESSION	AX548073												
VERSION	AX548073.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Conklin,D.C., Gao,Z., Lofton-Day,C.E. and Whitmore,T.E.												
TITLE	Secreted alpha-helical protein zlm2a24												
JOURNAL	Patent: WO 0234917-A 22 02-MAY-2002;												
FEATURES	ZymoGenetics, Inc. (US)												
source	Location/Qualifiers												
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ORIGIN													
Alignment Scores:													
Pred. No.:			8.33e+03	5.00	100.00%	2.53%	6	18 bp	5	0	0	0	0
Score:			5.00										
Percent Similarity:			100.00%										
Best Local Similarity:			100.00%										
Query Match:			2.53%										
DB:			6										
US-09-966-880A-8 (1-198) x AX548073 (1-18)													
QY	32	ValValLysArgArg	36										
Db	2	GTGTAAACGACGG	16										
RESULT 162													
LOCUS	AX713216/c												
DEFINITION	Sequence 102 from Patent WO03018837.												
ACCESSION	AX713216												
VERSION	AX713216.1												
KEYWORDS	synthetic construct												
SOURCE	synthetic construct												
ORGANISM	artificial sequences.												
REFERENCE	1												
AUTHORS	Waschuetza,S., Schnakenberg,E. and Lustig,M.												
TITLE	Method and diagnostic kit for the molecular diagnosis of												

/note="primer"

## ORIGIN

Alignment Scores: 18  
 Pred. No.: 8.33e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX802807 (1-18)

QY 174 ArgGlnLeuArgArg 178  
 |||||  
 DB 18 AGACAGCTCAGAAGA 4

## RESULT 165

AX803113/c 18 bp DNA linear PAT 24-NOV-2003  
 LOCUS AX803113  
 DEFINITION Sequence 145 from Patent WO03057927.  
 ACCESSION AX803113  
 VERSION AX803113.1 GI:38501778

KEYWORDS Human papillomavirus  
 SOURCE Human papillomavirus

ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 Papillomavirus.

REFERENCE 1  
 AUTHORS Karlsen,F.  
 TITLE Detection of human papillomavirus e6 mrna  
 JOURNAL Patent: WO 03057927-A 145 17-JUL-2003;  
 Norchip A/S (NO)

FEATURES  
 source  
 1..18  
 Location/Qualifiers  
 /organism="Human papillomavirus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:10566"

## ORIGIN

Alignment Scores: 18  
 Pred. No.: 8.33e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX803113 (1-18)

QY 174 ArgGlnLeuArgArg 178  
 |||||  
 DB 18 AGACAGCTCAGAAGA 4

## RESULT 166

AX803298/c 18 bp DNA linear PAT 24-NOV-2003  
 LOCUS AX803298  
 DEFINITION Sequence 330 from Patent WO03057927.  
 ACCESSION AX803298

VERSION AX803298.1 GI:38501963  
 SOURCE Human papillomavirus

ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 Papillomavirus.

REFERENCE 1  
 AUTHORS Karlsen,F.  
 TITLE Detection of human papillomavirus e6 mrna  
 JOURNAL Patent: WO 03057927-A 330 17-JUL-2003;  
 Norchip A/S (NO)

FEATURES  
 source  
 1..18  
 Location/Qualifiers  
 /organism="Human papillomavirus"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:10566"

## ORIGIN

Alignment Scores: 18  
 Pred. No.: 8.33e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX803298 (1-18)

QY 174 ArgGlnLeuArgArg 178  
 |||||  
 DB 18 AGACAGCTCAGAAGA 4

## RESULT 167

BD006571 18 bp DNA linear PAT 31-JAN-2002  
 LOCUS BD006571  
 DEFINITION Secreted salivary ZSIG32 polypeptides.  
 ACCESSION BD006571

VERSION BD006571.1 GI:18634942  
 KEYWORDS JP 2001501834-A/10.

SOURCE unidentified  
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Sheppard,P.O.  
 TITLE Secreted salivary ZSIG32 polypeptides  
 JOURNAL Patent: JP 2001501834-A 10 13-FEB-2001;  
 ZYMOGENETICS INC

COMMENT  
 OS Unidentified  
 PN JP 2001501834-A/10  
 PD 13-FEB-2001  
 PF 18-MAR-1998 JP 1998540741  
 PR 19-MAR-1997 US 60/041263  
 PI PAUL O SHEPPARD  
 PC C12N15/12,C07K14/47,A61K38/17,C07K16/18,C12Q1/68,C12N15/62, PC  
 C12N15/11

PC G01N33/50  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..18  
 FT /organism='Unidentified'.

FEATURES  
 source  
 1..18  
 Location/Qualifiers  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Alignment Scores: 18  
 Pred. No.: 8.33e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD006571 (1-18)

QY 32 ValVallysArgArg 36  
 |||||  
 DB 2 GTTGTAACGACGG 16

## RESULT 168

BD073403 18 bp DNA linear PAT 27-AUG-2002  
 LOCUS BD073403  
 DEFINITION Secreted protein which human chromosome 13 encodes.

ACCESSION BD073403

```

VERSION BD073403.1 GI:22619006
KEYWORDS JP 2001511345-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
         artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O. and Gilberton,D.G.
TITLE Secreted protein which human chromosome 13 encodes
JOURNAL Patent: JP 2001511345-A 2 14-AUG-2001;
        ZYMOGENETICS INC
COMMENT OS Artificial Sequence
        PN JP 2001511345-A/2
        PD 14-AUG-2001
        PF 24-JUL-1998 JP 2000504249
        PR 24-JUL-1997 US 60/053613
        PI PAUL O SHEPPARD,DIBRA G GILBERTON
        PC C12N15/09,A61K38/00,A61K48/00,C07K14/47,C07K16/18,C12N1/15,PC
        C12N1/19,
        PC
C12N1/21,C12N5/10,C12P21/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/PC
00
CC Oligonucleotide ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
  source      Location/Qualifiers
  1..18       /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0

US-09-966-880A-8 (1-198) x BD074786 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAACGACGG 16

RESULT 170
BD095308
LOCUS      BD095308
DEFINITION The method of testing for psoriasis vulgaris.
ACCESSION BD095308
VERSION   BD095308.1 GI:22640896
KEYWORDS  WO 0142458-A/13.
SOURCE    synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Inoko,H. and Tamiya,G.
TITLE     The method of testing for psoriasis vulgaris
JOURNAL   Patent: WO 0142458-A 13 14-JUN-2001;
          HIDEOSHI INOKO,GEN TAMIYA
COMMENT   OS Artificial Sequence
          PN WO 0142458-A/13
          PD 14-JUN-2001
          PF 06-DEC-2000 WO 2000JP008624
          PR 06-DEC-1999 JP 99P 346867
          PI HIDEOSHI INOKO,GEN TAMIYA
          PC C12N15/12,C12Q1/68
          CC Description of Artificial Sequence:an artificially synthesized

CC      sequence
FH      Key Location/Qualifiers
FT      source 1..18
FT /organism='Artificial Sequence'.

FEATURES
  source      Location/Qualifiers
  1..18       /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0

US-09-966-880A-8 (1-198) x BD095308 (1-18)

QY      128 ArgLeuHisArgAla 132
Db      4 CGCCTCCACAGAGCT 18

RESULT 169
BD074786
LOCUS      BD074786
DEFINITION Homolog of protein specific to adipocyte.
ACCESSION BD074786
VERSION   BD074786.1 GI:22620389
KEYWORDS  JP 2001513998-A/5.
SOURCE    synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Sheppard,P.O. and Humes,J.M.
TITLE     Homolog of protein specific to adipocyte
JOURNAL   Patent: JP 2001513998-A 5 11-SEP-2001;
          ZYMOGENETICS INC
COMMENT   OS Artificial Sequence
        PN JP 2001513998-A/5
        PD 11-SEP-2001
        PF 26-AUG-1998 JP 2000507800
        PR 26-AUG-1997 US 60/056983
        PI PAUL O SHEPPARD,JACQUELINE M HUMES
        PC C12N15/09,A61K38/17,A61K39/395,A61K45/00,A61P29/00,
        A61P43/00,
        PC
        PC C07K14/47,C07K16/18,C12P21/02,C12Q1/68//C12P21/08,C12N15/00,
        A61K37/12
        PC
        CC Oligonucleotide ZC976
        FH Key Location/Qualifiers

```

```
RESULT 171
BD160908
LOCUS       BD160908                18 bp    DNA        linear        PAT 17-JAN-2003
DEFINITION   Gene Hd3a deriving flowering of plant and utilization thereof.
ACCESSION    BD160908
VERSION      BD160908.1 GI:278666666
KEYWORDS     JP 2002153283-A/20.
SOURCE       synthetic construct
ORGANISM     artificial construct
REFERENCE    1 (bases 1 to 18)
AUTHORS      Yano,M. and Kojima,A.
TITLE        Gene Hd3a deriving flowering of plant and utilization thereof
JOURNAL      Patent: JP 2002153283-A 20 28-MAY-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES
MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, BIO ORIENTED
TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION, SOCIETY FOR TECHNO
INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
COMMENT      OS Artificial Sequence
FN          JP 2002153283-A/20
PD          28-MAY-2002
PF          24-NOV-2000 JP 2000356839
PI          MASAHIRO YANO,AKIKO KOJIMA
PC          C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N15/09,C12R1:91), PC
              (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N15/00,C12R1:91), PC
              (C12N5/00,C12R1:91)
CC          Description of Artificial Sequence:an artificially synthesized

FEATURES             source
    CC          sequence          primer
    FH          key               Location/Qualifiers
    FT          source            1..18
                                  /organism='Artificial Sequence'.
FEATURES             source
    CC          sequence          primer
    FH          key               Location/Qualifiers
    FT          source            1..18
                                  /organism='Artificial Sequence'.
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:        0
DB:              6           Gaps:         0

US-09-966-880A-8 (1-198) x BD169088 (1-18)

QY          38 SerAlaThrSerPhe 42
          |||||
          4 TCAGCAACGAGTTTC 18
          /organism='Artificial Sequence'.
          /db_xref='taxon:32630'

RESULT 173
BD206032
LOCUS       BD206032                18 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION   Soluble protein ZTMPO-1.
ACCESSION    BD206032
VERSION      BD206032.1 GI:33015802
KEYWORDS     JP 2002512033-A/7.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Sheppard,P.O., Conklin,D.C., Farrah,T.M., Maurer,M.F. and
              Grossmann,A.
TITLE        Soluble protein ZTMPO-1
JOURNAL      Patent: JP 2002512033-A 7 23-APR-2002;
              ZYMOGENETICS INC
COMMENT      OS Artificial Sequence
          PN          JP 2002512033-A/7
          PD          23-APR-2002
          PF          19-APR-1999 JP 2000544800
          PR          21-APR-1998 US 09/063838
          PI          PAUL O SHEPPARD,DARRELL C CONKLIN,THERESA M FARRAH,MARK F PI
              MAURER,
              PI ANGELIKA GROSSMANN
              PC C12N15/09,A61K38/22,A61P43/00,C07K14/66,C07K16/26,
              PC C07K19/00,
              PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/
              68//
              PC A61K39/395,A61K39/395,C12N15/00,A61K37/02,A61K37/24,C12N5/00
              CC Oligonucleotide ZC976
              FT          key               Location/Qualifiers
              FT          source            1..18
                                  /organism='Artificial Sequence'.
              /db_xref='taxon:32630'

FEATURES             source
    CC          sequence          primer
    FH          key               Location/Qualifiers
    FT          source            1..18
                                  /organism='Artificial Sequence'.
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:        0
DB:              6           Gaps:         0

US-09-966-880A-8 (1-198) x BD160908 (1-18)

QY          38 SerAlaThrSerPhe 42
          |||||
          4 TCAGCAACGAGTTTC 18
          /organism='Artificial Sequence'.
          /db_xref='taxon:32630'

RESULT 172
BD169088
LOCUS       BD169088                18 bp    DNA        linear        PAT 17-JAN-2003
DEFINITION   Gene Hd3a inducing plant flowering and utilization thereof.
ACCESSION    BD169088
VERSION      BD169088.1 GI:27874900
KEYWORDS     WO 0242475-A/20.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Yano,M. and Kojima,S.
TITLE        Gene Hd3a inducing plant flowering and utilization thereof
JOURNAL      Patent: WO 0242475-A 20 30-MAY-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES, BIO ORIENTED
TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION, MASAHIRO YANO, SHOKO
KOJIMA
COMMENT      OS Artificial Sequence
          PN          WO 0242475-A/20
```



```
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD206032 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 174
BD211410
LOCUS BD211410 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Immunomodulator polypeptide ZSIG57.
ACCESSION BD211410
VERSION BD211410.1 GI:33021180
KEYWORDS JP 2002518009-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O.
TITLE Immunomodulator polypeptide ZSIG57
JOURNAL Patent: JP 2002518009-A 3 25-JUN-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002518009-A/3
PD 25-JUN-2002
PF 20-MAY-1999 JP 2000554849
PR 18-JUN-1998 US 09/099600
PI PAUL O SHEPPARD
PC C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12B21/08//C12N1/19,C12R1/84,C12N15/00,C12N5/00 CC
Oligonucleotide primer Zc976
FH Key Location/Qualifiers
FT source 1..18
FT /organism="Artificial Sequence".
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD211410 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 175
AR002659
LOCUS AR002659 19 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 20 from patent US 5741957.
ACCESSION AR002659
VERSION AR002659.1 GI:3964213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Deboer,H.A., Strijker,R., Heyneker,H.L., Platenburg,G., Lee,S.He.,

Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR002659 (1-19)

QY 32 ValVallysArgArg 36
Db 5 GTTGTAAACGACGG 19

RESULT 176
AR065110
LOCUS AR065110 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5849486.
ACCESSION AR065110
VERSION AR065110.1 GI:5995326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Heller,M.James., O'Connell,J.Patrick., Juncosa,R.David.,
Soszowski,R.George, and Jackson,T.Ratcliffe.
TITLE Methods for hybridization analysis utilizing electrically
controlled hybridization
JOURNAL Patent: US 5849486-A 2 15-DEC-1998;
FEATURES
source
1..19
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR065110 (1-19)

QY 56 HisValGluLeuLeu 60
Db 2 CACGTAGAACTGCTC 16

RESULT 177
AR118403
LOCUS AR118403 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6140552.
ACCESSION AR118403
VERSION AR118403.1 GI:14099309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Deboer,H.A., Strijker,R., Heyneker,H.L., Platenburg,G., Lee,S.He.,
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Pieper, P. and Krimpenfort, P.J.A.
Production of recombinant polypeptides by bovine species and
transgenic methods
JOURNAL Patent: US 6140552-A 20 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:      Length:      19
Pred. No.:      8.73e+03      Matches:      5
Score:      5.00      Conservative:      0
Percent Similarity:      100.00%      Mismatches:      0
Best Local Similarity:      100.00%      Indels:      0
Query Match:      2.53%      Gaps:      0
DB:
US-09-966-880A-8 (1-198) x AR118403 (1-19)

QY      32 ValVallysArgArg 36
      |||||
Db      5 GTTGTAAACGACGG 19

RESULT 178
LOCUS      AR153868      19 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION      Sequence 21 from patent US 6238624.
ACCESSION      AR153868
VERSION      AR153868.1 GI:15121921
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Heller, M.J., Tu, E., Evans, G.A. and Sosnowski, R.G.
TITLE      Methods for transport in molecular biological analysis and
diagnostics
JOURNAL Patent: US 6238624-A 21 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:      Length:      19
Pred. No.:      8.73e+03      Matches:      5
Score:      5.00      Conservative:      0
Percent Similarity:      100.00%      Mismatches:      0
Best Local Similarity:      100.00%      Indels:      0
Query Match:      2.53%      Gaps:      0
DB:
US-09-966-880A-8 (1-198) x AR153868 (1-19)

QY      56 HisValGluLeuLeu 60
      |||||
Db      2 CACGTAGACTGCTC 16

RESULT 179
LOCUS      AR157371      19 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION      Sequence 2 from patent US 6245508.
ACCESSION      AR157371
VERSION      AR157371.1 GI:16218306
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Heller, M.J., Tu, E., Evans, G.A. and Sosnowski, R.G.
TITLE      Method for fingerprinting utilizing an electronically addressable
array

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JOURNAL Patent: US 6245508-A 2 12-JUN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:      Length:      19
Pred. No.:      8.73e+03      Matches:      5
Score:      5.00      Conservative:      0
Percent Similarity:      100.00%      Mismatches:      0
Best Local Similarity:      100.00%      Indels:      0
Query Match:      2.53%      Gaps:      0
DB:
US-09-966-880A-8 (1-198) x AR157371 (1-19)

QY      56 HisValGluLeuLeu 60
      |||||
Db      2 CACGTAGACTGCTC 16

RESULT 180
LOCUS      E36205/C      19 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION      Process for preparing ammonia oxidizing bacterium variant with
limited proliferation in natural environment.
ACCESSION      E36205
VERSION      E36205.1 GI:13022532
KEYWORDS      JP 1999235188-A/7.
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1 (bases 1 to 19)
AUTHORS      Taro, I.
TITLE      Process for preparing ammonia oxidizing bacterium variant with
limited proliferation in natural environment
JOURNAL Patent: JP 1999235188-A 7 31-AUG-1999;
COMMENT      KURIYA WATER IND LTD
OS      Unidentified
PN      JP 1999235188-A/7
PD      31-AUG-1999
PF      08-DEC-1998 JP 1998349146
PR      TARO IZUMI
PC      C12N15/09 C12N1/21//C12N9/88, (C12N1/21, C12R1:01), C12N15/00 CC
Strandedness: Single;
CC      Topology: Linear;
FH      Key      Location/Qualifiers
FT      source 1..19
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:      Length:      19
Pred. No.:      8.73e+03      Matches:      5
Score:      5.00      Conservative:      0
Percent Similarity:      100.00%      Mismatches:      0
Best Local Similarity:      100.00%      Indels:      0
Query Match:      2.53%      Gaps:      0
DB:
US-09-966-880A-8 (1-198) x E36205 (1-19)

QY      32 ValVallysArgArg 36
      |||||
Db      15 GTTGTAAACGACGG 1

RESULT 181
E37237/C

```

LOCUS	E37237	19 bp	DNA	linear	PAT 31-JAN-2000
DEFINITION	Method for evaluating nitrification inhibitory activity of drain on activated sludge.				
ACCESSION	E37237				
VERSION	E37237.1	GI:18626644			
KEYWORDS	JP 2000184898-A/4.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Izumai, T.				
TITLE	Method for evaluating nitrification inhibitory activity of drain on activated sludge				
JOURNAL	Patent: JP 2000184898-A 4 04-JUL-2000;				
COMMENT	KURITA WATER IND LTD				
	OS	Unidentified			
	PN	JP 2000184898-A/4			
	PD	04-JUL-2000			
	PF	21-DEC-1998	JP 1998362680		
	PR	TARO IZUMI			
	PI	CI2Q1/02, C02F3/12, C02F3/34, C12N1/21, C12N15/09//G01N33/18, PC			
	CC	(C12N1/21, C12R1:01), C12N15/00			
	CC	Strandedness: Single;			
	CC	Topology: Linear;			
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	FT	source	1..19		
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FEATURES	Location/Qualifiers				
source	1..19				
	/organism="unidentified"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32644"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.73e-03	Length:	19		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x E37237 (1-19)					
Qy	32	ValValValysArg	36		
Db	15	GTTGTAACGACGG	1		
RESULT 182					
II17625/c					
LOCUS	II17625	19 bp	DNA	linear	PAT 07-OCT-1996
DEFINITION	Sequence 17 from patent US 5491225.				
ACCESSION	II17625				
VERSION	II17625.1	GI:1597980			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Picone, T.K.H., McCallum, T.M. and Zoccoli, M.A.				
TITLE	PCR primers for detection of legionella species and methods for controlling visual intensity in hybridization assays				
JOURNAL	Patent: US 5491225-A 17-13-FEB-1996;				
FEATURES	Location/Qualifiers				
source	1..19				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.73e-03	Length:	19		
Score:	5.00	Matches:	5		

Qy	82 ThrSerTrpSerPro 86 
Db	17 ACAAGCTGGAGCCCA 3 
RESULT 187	
I88976/c	I88976 linear PAT 10-AUG-1998
LOCUS	Sequence 18 from patent US 5719271.
DEFINITION	Sequence 18 from patent US 5719271.
ACCESSION	I88976
VERSION	I88976.1 GI:3408916
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 19) Cook,P.Dan., Manoharan,M. and Bruice,T. Covalently cross-linked oligonucleotides JOURNAL Patent: US 5719271-A 18 FEB-1998; FEATURES Location/Qualifiers source 1..19 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	
Pred. NO.:	8.73e+03 Length: 19
Score:	5.00 Matches: 5
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	2.53% Indels: 0
DB:	Gaps: 0
US-09-966-880A-8 (1-198) x I88976 (1-19)	
Qy	179 IleIeuLeuProIeu 183 
Db	17 ATTTCCTACCTCTG 3 
RESULT 188	
AR222934	AR222934 linear PAT 26-SEP-2002
LOCUS	Sequence 44 from patent US 6432639.
DEFINITION	Sequence 44 from patent US 6432639.
ACCESSION	AR222934
VERSION	AR222934.1 GI:23330771
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 19) Lichter,J.B. and Guida,M. Isolated CYP3A4 nucleic acid molecules and detection methods JOURNAL Patent: US 6432639-A 44 13-AUG-2002, FEATURES Location/Qualifiers source 1..19 /organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Alignment Scores:	
Pred. NO.:	8.73e+03 Length: 19
Score:	5.00 Matches: 5
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	2.53% Indels: 0
DB:	Gaps: 0
US-09-966-880A-8 (1-198) x AR222934 (1-19)	
Qy	22 LysGlyArgGlu 26 
Db	3 AAGGCAGAGAGAG 17 
RESULT 189	

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AR364956/c
LOCUS AR364956 19 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5455029.
ACCESSION AR364956
VERSION AR364956.1 GI:34428177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Unclassified.
AUTHORS Hartman,J.R., Oppenheim,A.B., Gorecki,M., Aviv,H. and Oren,R.
TITLE Therapeutic compositions comprising a mixture of human CuZn
  superoxide dismutase analogs
JOURNAL Patent: US 5455029-A 5 03-OCT-1995;
FEATURES
  source Location/Qualifiers
    1..19
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR364956 (1-19)
QY 69 AspLeuAspProGly 73
Db 18 GATCTAGACCGGGA 4
RESULT 190
AR364974/c
LOCUS AR364974 19 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 25 from patent US 5455029.
ACCESSION AR364974
VERSION AR364974.1 GI:34428195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Unclassified.
AUTHORS Hartman,J.R., Oppenheim,A.B., Gorecki,M., Aviv,H. and Oren,R.
TITLE Therapeutic compositions comprising a mixture of human CuZn
  superoxide dismutase analogs
JOURNAL Patent: US 5455029-A 25 03-OCT-1995;
FEATURES
  source Location/Qualifiers
    1..19
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR364974 (1-19)
QY 69 AspLeuAspProGly 73
Db 18 GATCTAGACCGGGA 4
RESULT 191
AR430797
LOCUS AR430797 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 100 from patent US 6649409.
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AR430797
ACCESSION AR430797.1 GI:40191726
VERSION AR430797.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Unclassified.
AUTHORS Fomsgaard,A.
TITLE Method for producing a nucleotide sequence construct with optimized
  codons for an HIV genetic vaccine based on a primary, early HIV
  isolate and synthetic envelope BX08 constructs
JOURNAL Patent: US 6649409-A 100 18-NOV-2003;
FEATURES
  source Location/Qualifiers
    1..19
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    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR430797 (1-19)
QY 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15
RESULT 192
AXI29047
LOCUS AXI29047 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 265 from Patent WO0130362.
ACCESSION AXI29047
VERSION AXI29047.1 GI:14135352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  Robbins,J.M. and Tritz,R.
  Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
JOURNAL Patent: WO 0130362-A 265 03-MAY-2001;
FEATURES
  source Location/Qualifiers
    1..19
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
    /note="Cdk2 ribozyme binding site"
ORIGIN
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AXI29047 (1-19)
QY 193 PheArgThrLeuGly 197
Db 1 TTTCGGACTCTGGGG 15
RESULT 193
AXI30454
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LOCUS AX130454 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 1672 from Patent WO0130362.  
ACCESSION AX130454  
VERSION AX130454.1 GI:14136759  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Robbins J.M. and Tritz, R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 1672 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cyclin C ribozyme binding site"  
ORIGIN  
Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX130454 (1-19)  
QY 62 LeuArgTyrIleSer 66  
Db 3 CTACGGTATATTCA 17  
RESULT 194  
AX130455  
LOCUS AX130455 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 1673 from Patent WO0130362.  
ACCESSION AX130455  
VERSION AX130455.1 GI:14136760  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Robbins J.M. and Tritz, R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 1673 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cyclin C ribozyme binding site"  
ORIGIN  
Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX130455 (1-19)  
QY 62 LeuArgTyrIleSer 66  
Db 3 CTACGGTATATTCA 17

LOCUS AX130454 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 1672 from Patent WO0130362.  
ACCESSION AX130454  
VERSION AX130454.1 GI:14136759  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Robbins J.M. and Tritz, R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 1672 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES source  
1. .19  
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/db\_xref="taxon:9606"  
/note="Cyclin C ribozyme binding site"  
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Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX130454 (1-19)  
QY 62 LeuArgTyrIleSer 66  
Db 3 CTACGGTATATTCA 17

LOCUS AX130455 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 1673 from Patent WO0130362.  
ACCESSION AX130455  
VERSION AX130455.1 GI:14136760  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Robbins J.M. and Tritz, R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 1673 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cyclin C ribozyme binding site"  
ORIGIN  
Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX130455 (1-19)  
QY 62 LeuArgTyrIleSer 66  
Db 3 CTACGGTATATTCA 17

LOCUS AX421255 19 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 3 from Patent WO0218641.  
ACCESSION AX421255  
VERSION AX421255.1 GI:21524663  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Claissan, E.  
TITLE Detection of CYP3A4 and CYP2C9 polymorphisms  
JOURNAL Patent: WO 0218641-A 3 07-MAR-2002;  
Geminl Genomics PLC (GB)  
FEATURES source  
1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide of CYP3A4 region"  
ORIGIN  
Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX421255 (1-19)  
QY 22 LysGlyArgArgGlu 26  
Db 3 AAGGGCAGGAGAGAG 17  
RESULT 196  
AX497578  
LOCUS AX497578 19 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 122 from Patent WO0233126.  
ACCESSION AX497578  
VERSION AX497578.1 GI:23342848  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Grenier, J.K., Marshall, D.J., Prudent, J.R., Richmond, C.S.,  
Roesch, E.B., Scherrer, C.W., Sherrill, C.B. and Ptacin, J.L.  
TITLE Solid support assay systems and methods utilizing non-standard bases  
JOURNAL Patent: WO 0233126-A 122 25-APR-2002;  
Eragen Biosciences, Inc. (US)  
FEATURES source  
1. .19  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic Oligonucleotides"  
ORIGIN  
Alignment Scores: 8.73e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6  
US-09-966-880A-8 (1-198) x AX421255 (1-19)  
QY 22 LysGlyArgArgGlu 26  
Db 3 AAGGGCAGGAGAGAG 17

US-09-966-880A-8 (1-198) x AX497578 (1-19)

QY 111 AlaArgLeuTyrPhe 115  
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 Db 1 GCAAGGCTCTACTTC 15

# RESULT 197

AX708353  
 LOCUS AX708353 19 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 12 from Patent WO02074952.  
 ACCESSION AX708353  
 VERSION AX708353.1 GI:29564240  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Merk, H. and Stiege, W.  
 TITLE Nucleic acid which is stabilised against decomposition  
 JOURNAL Patent: WO 02074952-A 12 26-SEP-2002;  
 Rina Network RNA-Technologien GmbH (DE)  
 FEATURES Location/Qualifiers  
 source  
 primer\_bind  
 1..19  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.73e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX708353 (1-19)

QY 32 ValVallysArgArg 36  
 |||||  
 Db 5 GTTGTAACGACGG 19

# RESULT 198

AX708367  
 LOCUS AX708367 19 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 12 from Patent WO02090371.  
 ACCESSION AX708367  
 VERSION AX708367.1 GI:29564254  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Merk, H., Erdmann, V. and Stiege, W.  
 TITLE Method for preparative production of long nucleic acids by PCR  
 JOURNAL Patent: WO 02090371-A 12 14-NOV-2002;  
 Rina Network RNA-Technologien GmbH (DE)  
 FEATURES Location/Qualifiers  
 source  
 primer\_bind  
 1..19  
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 /db\_xref="taxon:32630"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.73e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX708367 (1-19)

QY 32 ValVallysArgArg 36  
 |||||  
 Db 5 GTTGTAACGACGG 19

# RESULT 199

AX710980  
 LOCUS AX710980 19 bp RNA linear PAT 11-APR-2003  
 DEFINITION Sequence 280 from Patent EP1288296.  
 ACCESSION AX710980  
 VERSION AX710980.1 GI:29787361  
 KEYWORDS Human herpesvirus 5  
 SOURCE Human herpesvirus 5  
 ORGANISM Human herpesvirus 5  
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 Betaherpesvirinae; Cytomegalovirus.  
 REFERENCE 1  
 AUTHORS Draper, K.G., McSwiggen, J.A., Holecek, J.J., Dudycz, L.W.,  
 Macejak, D.G. and Mamone, J.A.  
 TITLE Method and reagent for inhibiting HBV viral replication  
 JOURNAL Patent: EP 1288296-A 280 05-MAR-2003;  
 RIBOZYME PHARMACEUTICALS, INC. (US)  
 FEATURES Location/Qualifiers  
 source  
 1..19  
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 /db\_xref="taxon:10359"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.73e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX710980 (1-19)

QY 124 GluGlyLeuArgArg 128  
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 Db 1 GAAGGCTACGCGT 15

# RESULT 200

BD001121  
 LOCUS BD001121 19 bp RNA linear PAT 31-JAN-2002  
 DEFINITION Method and reagent for inhibiting viral replication.  
 ACCESSION BD001121  
 VERSION BD001121.1 GI:18625680  
 KEYWORDS JP 2000342285-A/281.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Draper, K.G., Dadykztz, L.W., Macswigen, J.A., Maysejak, D.G.,  
 Holecek, J.J. and Mamone, A.J.  
 TITLE Method and reagent for inhibiting viral replication  
 JOURNAL Patent: JP 2000342285-A 281 12-DEC-2000;  
 RIBOZYME PHARMACEUTICALS INC  
 COMMENT OS Artificial Sequence  
 PN JP 2000342285-A/281  
 PD 12-DEC-2000  
 PF 01-MAY-2000 JP 2000132616  
 PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR  
 14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR  
 14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR  
 14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR  
 14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR  
 14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR  
 14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR  
 14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR

PI	JAMES J HOLESEK, ANTHONY J MAMONE
PC	C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC	A61K39/135,
PC	A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC	A61P1/16,
PC	A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
	(C12N15/09, C12R1:93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
	C12R1:93)
CC	
Key	Location/Qualifiers
FT	1. .19
FT	/organism='Artificial Sequence'
FEATURES	
source	Location/Qualifiers
	1. .19
	/organism="synthetic construct"
	/mol_type="genomic RNA"
	/db_xref="taxon:32630"
ORIGIN	
Alignment Scores:	
Pred. No.:	8.73e+03 Length: 19
Score:	5.00 Matches: 5
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	2.53% Indels: 0
DB:	6 Gaps: 0
US-09-966-880A-8 (1-198) x BD001550 (1-19)	
QY	124 GluGlyLeuArgArg 128
Db	1 GAAGGCCTACGCCGT 15
RESULT 202	
BD087510	
LOCUS	BD087510 19 bp DNA linear PAT 27-AUG-2002
DEFINITION	Self-assembling microelectronic integration system capable of
	designation self address, compartment device, mechanism, method and
	operation for molecular biological analysis and diagnosis.
ACCESSION	BD087510
VERSION	BD087510.1 GI:22633120
KEYWORDS	JP 2001525193-A/21.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Sosnowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
AUTHORS	Edman, C.F.
TITLE	Self-assembling microelectronic integration system capable of
	designation self address, compartment device, mechanism, method and
	operation for molecular biological analysis and diagnosis
JOURNAL	Patent: JP 2001525193-A 21 11-DEC-2001;
	NANOGEN INC
COMMENT	OS Homo sapiens (human)
	EN JP 2001525193-A/21
	PD 11-DEC-2001
	PF 01-DEC-1998 JP 2000524303
	PR 05-DEC-1997 US 08/986085
	PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
	NERENBERG,
	PI MICHAEL J HELLER, CARL F EDMAN
	PC C12Q1/68, C12N15/09, C12N15/00
	CC Self-assembling microelectronic integration system capable of
	designating
	CC self address, compartment device, mechanism, method and CC
	operation for
	CC molecular biological analysis and diagnosis
FT	Key Location/Qualifiers
FT	1. .19
FT	/organism='Homo sapiens (human)'
FEATURES	
source	Location/Qualifiers
	1. .19



/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.73e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD087510 (1-19)

Qy 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16  
|||||

## RESULT 203

BD087534/c

## LOCUS

DEFINITION BD087534 19 bp DNA linear PAT 27-AUG-2002  
Self-assembling microelectronic integration system capable of  
designating self address, compartment device, mechanism, method and  
operation for molecular biological analysis and diagnosis.

## ACCESSION

BD087534

VERSION BD087534.1 GI:22633144

KEYWORDS JP 2001525193-A/45.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS Sosnowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and Edman, C.F.

TITLE Self-assembling microelectronic integration system capable of

designating self address, compartment device, mechanism, method and

operation for molecular biological analysis and diagnosis

Patent: JP 2001525193-A 45 11-DEC-2001;

NANOGEN INC

COMMENT OS Homo sapiens (human)

PN JP 2001525193-A/45

PD 11-DEC-2001

PF 01-DEC-1998 JP 2000524303

PR 05-DEC-1997 US 08/986065

PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI

NERENBERG,

PI MICHAEL J HELLER, CARL F EDMAN

PC C1201/68, C12N15/09, C12N15/00

CC Self-assembling microelectronic integration system capable of

designating

CC self address, compartment device, mechanism, method and CC

operation for

CC molecular biological analysis and diagnosis

FT Key Location/Qualifiers

FT source 1..19

FT Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.73e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD087534 (1-19)

Qy 56 HisValGluLeuLeu 60  
|||||  
Db 18 CACGTAGACTGCTC 4

## RESULT 204

BD087539/c

## LOCUS

DEFINITION BD087539 19 bp DNA linear PAT 27-AUG-2002  
Self-assembling microelectronic integration system capable of  
designating self address, compartment device, mechanism, method and  
operation for molecular biological analysis and diagnosis.

## ACCESSION

BD087539

VERSION BD087539.1 GI:22633149

KEYWORDS JP 2001525193-A/50.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS Sosnowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and Edman, C.F.

TITLE Self-assembling microelectronic integration system capable of

designating self address, compartment device, mechanism, method and

operation for molecular biological analysis and diagnosis

Patent: JP 2001525193-A 50 11-DEC-2001;

NANOGEN INC

COMMENT OS Homo sapiens (human)

PN JP 2001525193-A/50

PD 11-DEC-2001

PF 01-DEC-1998 JP 2000524303

PR 05-DEC-1997 US 08/986065

PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI

NERENBERG,

PI MICHAEL J HELLER, CARL F EDMAN

PC C1201/68, C12N15/09, C12N15/00

CC Self-assembling microelectronic integration system capable of

designating

CC self address, compartment device, mechanism, method and CC

operation for

CC molecular biological analysis and diagnosis

FT Key Location/Qualifiers

FT source 1..19

FT Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.73e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD087539 (1-19)

Qy 56 HisValGluLeuLeu 60

Db 18 CACGTAGACTGCTC 4  
|||||

## RESULT 205

A00694

## LOCUS

DEFINITION A00694 20 bp DNA linear PAT 22-MAR-1993  
Artificial sequence for controllable repressor operator (HO -150).

## ACCESSION

A00694

VERSION A00694.1 GI:344205

KEYWORDS

SOURCE synthetic construct

ORGANISM

REFERENCE	ORGANISM	synthetic construct artificial sequences.	1 (bases 1 to 20)	PAT 07-MAR-1997
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
ORIGIN				
Alignment Scores:				
Pred. No.:		9.13e+03	Length: 20	
Score:		5.00	Matches: 5	
Percent Similarity:		100.00%	Conservative: 0	
Best Local Similarity:		100.00%	Mismatches: 0	
Query Match:		2.53%	Indels: 0	
DB:		6	Gaps: 0	
US-09-966-880A-8 (1-198) x A00694 (1-20)				
QY	192	AlaPheArgThrLeu 196		
Db	1	GCCTTTAGAACGCTT 15		
RESULT 206				
LOCUS	A07599	20 bp DNA linear		
DEFINITION		Synthetic antisense oligonucleotide (5604-5623).		
ACCESSION	A07599			
VERSION	A07599.1	GI:413102		
KEYWORDS		synthetic construct		
SOURCE		artificial sequences.		
ORGANISM		1 (bases 1 to 20)		
REFERENCE				
AUTHORS		Kretschmer, A., Koelbl, H. and Prommer, W.		
TITLE		Antisense-oligonucleotides for inhibiting the transactivator target		
JOURNAL		sequence (TAR) and the synthesis of the transactivator protein		
COMMENT		(Tat) of HIV-1, and their use		
FEATURES		Patent: EP 0386563-A 6 12-SEP-1990;		
source		BAYER AG		
ORIGIN				
Alignment Scores:				
Pred. No.:		9.13e+03	Length: 20	
Score:		5.00	Matches: 5	
Percent Similarity:		100.00%	Conservative: 0	
Best Local Similarity:		100.00%	Mismatches: 0	
Query Match:		2.53%	Indels: 0	
DB:		6	Gaps: 0	
US-09-966-880A-8 (1-198) x A07599 (1-20)				
QY	10	LysPheLeuTyxGln 14		
Db	17	AAGTTTCTCTATCAA 3		
RESULT 207				
LOCUS	A32719	20 bp DNA linear		
DEFINITION		Synthetic capture probe for HPV6/HPV11 E7 gene.		
ACCESSION	A32719			
VERSION	A32719.1	GI:1567567		
KEYWORDS		synthetic construct		
SOURCE				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
ORIGIN				
Alignment Scores:				
Pred. No.:		9.13e+03	Length: 20	
Score:		5.00	Matches: 5	
Percent Similarity:		100.00%	Conservative: 0	
Best Local Similarity:		100.00%	Mismatches: 0	
Query Match:		2.53%	Indels: 0	
DB:		6	Gaps: 0	
US-09-966-880A-8 (1-198) x A45733 (1-20)				
QY	32	ValVallysArgArg 36		
Db	2	GTGTGAAACGACGG 16		
RESULT 209				
LOCUS	A45737	20 bp DNA linear		
DEFINITION		Sequence 16 from Patent WO9520668.		
ACCESSION	A45737			
VERSION	A45737.1	GI:2300124		
KEYWORDS				
SOURCE				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
ORIGIN				
Alignment Scores:				
Pred. No.:		9.13e+03	Length: 20	
Score:		5.00	Matches: 5	
Percent Similarity:		100.00%	Conservative: 0	
Best Local Similarity:		100.00%	Mismatches: 0	
Query Match:		2.53%	Indels: 0	
DB:		6	Gaps: 0	
US-09-966-880A-8 (1-198) x A32719 (1-20)				
QY	174	ArgGlnLeuArgArg 178		
Db	1	AGACAGCTCAGAAGA 15		

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SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 20)
AUTHORS     Paul, W., Scott, R.J., Betzner, A., Huttner, E., Lenee, P. and Perez, P.
TITLE       METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
JOURNAL     Patent: WO 9520668-A 16 03-AUG-1995;
            NICKERSON BIOCEM LTD (GB)
COMMENT     Other publication CA 2182278 950803
            Other publication AU 1540995 950815.
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:        0
DB:             6            Gaps:          0
US-09-966-880A-8 (1-198) x A45737 (1-20)
QY           32 ValVallVsArgArg 36
DB           2 GTTGTAAACGACGG 16
RESULT 210
LOCUS       A45739
DEFINITION Sequence 18 from Patent WO9520668.
ACCESSION   A45739
VERSION     A45739.1 GI:2300126
KEYWORDS    unidentified
            unclassified
            ORGANISM
            1 (bases 1 to 20)
            Paul, W., Scott, R.J., Betzner, A., Huttner, E., Lenee, P. and Perez, P.
            METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
            Patent: WO 9520668-A 16 03-AUG-1995;
            NICKERSON BIOCEM LTD (GB)
            Other publication CA 2182278 950803
            Other publication AU 1540995 950815.
FEATURES    Location/Qualifiers
             source
               1..20
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:        0
DB:             6            Gaps:          0
US-09-966-880A-8 (1-198) x A45739 (1-20)
QY           32 ValVallVsArgArg 36
DB           2 GTTGTAAACGACGG 16
RESULT 211
LOCUS       A47817
DEFINITION Sequence 31 from Patent WO9533851.
ACCESSION   A47817
VERSION     A47817.1 GI:2301703
KEYWORDS    unidentified
            unclassified
            ORGANISM
            1 (bases 1 to 20)
            De.B.H., Portaeis, F., Machtelinckx, J., Jannes, G. and Rossau, R.
            METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF
            MYCOBACTERIUM SPECIES
            Patent: WO 9533851-A 31 14-DEC-1995;
            INNOGENETICS NV (BE)
            Other publication AU 2789695 960104.
FEATURES    Location/Qualifiers
             source
               1..20
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:        0
DB:             6            Gaps:          0
US-09-966-880A-8 (1-198) x A47817 (1-20)
QY           92 ArgHisValAlaAsp 96
DB           4 CGGCATGTCGGGAT 18
RESULT 212
LOCUS       AR011896/c
DEFINITION Sequence 49 from patent US 5763174.
ACCESSION   AR011896
VERSION     AR011896.1 GI:3969886
KEYWORDS    Unknown.
            Unclassified.
            ORGANISM
            1 (bases 1 to 20)
            Nishikura, K.
            RNA editing enzyme and methods of use thereof
            Patent: US 5763174-A 49 09-JUN-1998;
            JOURNAL
            Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:        0
DB:             6            Gaps:          0
US-09-966-880A-8 (1-198) x AR011896 (1-20)
QY           38 SerAlaThrSerPhe 42
DB           17 TCAGCCACATCCTTC 3
RESULT 213
LOCUS       AR020656/c
DEFINITION Sequence 44 from patent US 5789184.
ACCESSION   AR020656
VERSION     AR020656
KEYWORDS    linear
            PAT 07-MAR-1997
            PAT 04-DEC-1998
            PAT 05-DEC-1998
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VERSION AR020656.1 GI:3975271  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fowlkes,D.M., Broach,J., Manfredi,J., Klein,C., Murphy,A.J., Paul,J. and Trueheart,J.  
TITLE Yeast cells engineered to produce pheromone system protein surrogates, and uses therefor  
JOURNAL Patent: US 5789184-A 44 04-AUG-1998;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR020656 (1-20)  
Qy 104 LeuSerLeuArgIle 108  
Db 18 CTGAGTCTTCGATC 4  
RESULT 214  
LOCUS AR058897 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5837836.  
ACCESSION AR058897  
VERSION AR058897.1 GI:5984474  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Frederici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.  
TITLE Bovine beta.-mannosidase nucleic acid sequence  
JOURNAL Patent: US 5837836-A 3 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR058897 (1-20)  
Qy 179 IleLeuLeuProLeu 183  
Db 6 ATTCTTTTACCCGTG 20  
RESULT 215  
LOCUS AR060887 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5840875.  
ACCESSION AR060887  
VERSION AR060887.1 GI:5987337  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Schreiner,G.F., Meyer,T.W. and Oberbauer,R.  
TITLE Kidney Na/PO.sub.4 cotransporter antisense oligonucleotide  
JOURNAL Patent: US 5840875-A 2 24-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..20  
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/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR060887 (1-20)  
Qy 102 ProAsnLeuSerLeu 106  
Db 5 CCCAATCTCGCTG 19  
RESULT 216  
LOCUS AR061377 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 59 from patent US 5843653.  
ACCESSION AR061377  
VERSION AR061377.1 GI:5989068  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Gold,L. and Tuerk,C.  
TITLE Method for detecting a target molecule in a sample using a nucleic acid ligand  
JOURNAL Patent: US 5843653-A 59 01-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR061377 (1-20)  
Qy 32 ValValLysArgArg 36  
Db 4 GTTGTAAACGACGG 18  
RESULT 217  
LOCUS AR067127/C 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 475 from patent US 5851760.  
ACCESSION AR067127  
VERSION AR067127.1 GI:5998349  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Evans,G.A. and Smith,M.W.

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ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR080740 (1-20)

QY 181 LeuProLeuTyrGlu 185
|||||
Db 1 TTGCCCTTATGAG 15

RESULT 220
AR085526 20 bp DNA linear PAT 01-SEP-2000
LOCUS
DEFINITION Sequence 4 from patent US 5981731.
ACCESSION AR085526
VERSION AR085526.1 GI:10012293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P.
TITLE Antisense oligonucleotide modulation of B-raf gene expression
JOURNAL Patent: US 5981731-A 4 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR085526 (1-20)

QY 169 ServAlaArgLeuSer 173
|||||
Db 4 TCTGTAGGCTTCA 18

RESULT 221
AR099542 20 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 69 from patent US 6077833.
ACCESSION AR099542
VERSION AR099542.1 GI:12809308
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6077833-A 69 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:

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Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR099542 (1-20)

QY 176 LeuArgArgileu 180  
DB 1 CTGCGCGAATCCTG 15

RESULT 222  
AR108276  
LOCUS AR108276 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 59 from patent US 6110900.  
ACCESSION AR108276  
VERSION AR108276.1 GI:12823763  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Gold, L. and Tuerk, C.  
TITLE Nucleic acid ligands  
JOURNAL Patent: US 6110900-A 59 29-AUG-2000;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR108276 (1-20)

QY 32 ValVallysArgArg 36  
DB 4 GTTGTAACGACGG 18

RESULT 223  
AR112948  
LOCUS AR112948 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 34 from patent US 6132724.  
ACCESSION AR112948  
VERSION AR112948.1 GI:14093270  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Blum, X.  
TITLE Allelic polygene diagnosis of reward deficiency syndrome and treatment  
JOURNAL Patent: US 6132724-A 34 17-OCT-2000;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR112948 (1-20)

QY 22 LysGlyArgArgGlu 26  
DB 5 AAGGAGGAGGGAA 19

RESULT 224  
AR122465/c  
LOCUS AR122465 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 19 from patent US 6165728.  
ACCESSION AR122465  
VERSION AR122465.1 GI:14106782  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ward, D.T. and Cowser, L.M.  
TITLE Antisense modulation of NCK-2 expression  
JOURNAL Patent: US 6165728-A 19 26-DEC-2000;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR122465 (1-20)

QY 163 GluGlyLeuHisGlu 167  
DB 15 GAAGGACTCCATGAA 1

RESULT 225  
AR122466/c  
LOCUS AR122466 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 20 from patent US 6165728.  
ACCESSION AR122466  
VERSION AR122466.1 GI:14106783  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ward, D.T. and Cowser, L.M.  
TITLE Antisense modulation of NCK-2 expression  
JOURNAL Patent: US 6165728-A 20 26-DEC-2000;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR122466 (1-20)

```
Qy 163 GluGlyLeuHisGlu 167
Db 20 GAAGGACTCATGAA 6

RESULT 226
LOCUS ARI124504
DEFINITION Sequence 73 from patent US 6171860.
ACCESSION ARI124504
VERSION ARI124504.1 GI:14109865
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of rank expression
JOURNAL Patent: US 6171860-A 73 09-JAN-2001;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI124504 (1-20)

Qy 128 ArgLeuHisArgAla 132
Db 2 AGGTGCACCGGGCT 16

RESULT 227
LOCUS ARI130005
DEFINITION Sequence 7 from patent US 6187585.
ACCESSION ARI130005
VERSION ARI130005.1 GI:14117902
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Lipton,A. and Witters,L.M.
TITLE Oligonucleotide inhibition of epidermal growth factor receptor
JOURNAL expression
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI130005 (1-20)

Qy 129 LeuHisArgAlaGly 133
Db 6 TTGCACAGGCGAGGG 20

RESULT 228
LOCUS ARI136419
DEFINITION Sequence 14 from patent US 6136604.
ACCESSION ARI136419
VERSION ARI136419.1 GI:14477091
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Wyatt,J.
TITLE Antisense inhibition of methionine aminopeptidase 2 expression
JOURNAL Patent: US 6136604-A 14 24-OCT-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI136419 (1-20)

Qy 70 LeuAspProGlyArg 74
Db 6 CTGGATCCAGGTCGC 20

RESULT 229
LOCUS ARI136541
DEFINITION Sequence 31 from patent US 6136952.
ACCESSION ARI136541
VERSION ARI136541.1 GI:14477213
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Li,L. and Hood,L.
TITLE Human jagged polypeptide, encoding nucleic acids and methods of use
JOURNAL Patent: US 6136952-A 31 24-OCT-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI136541 (1-20)

Qy 27 ThrTyrLeuCysTyr 31
Db 16 ACATACCTCTGTAC 2

RESULT 230
LOCUS ARI137608
DEFINITION Sequence 2 from patent US 6197532.
ACCESSION ARI137608
```

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VERSION      ARI137608.1  GI:14479117
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Rao, P.N. and Raj, M.H.G.
TITLE       Diagnosis and detection of breast cancer and other cancers
JOURNAL     Patent: US 6197532-A 2 06-MAR-2001;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x ARI137608 (1-20)

Qy          179 IleLeuLeuProLeu 183
Db          19 ATCCTCTGCTCTG 5

RESULT 231
ARI146001
LOCUS       ARI146001          20 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 67 from patent US 6218150.
ACCESSION  ARI146001
VERSION    ARI146001.1  GI:15109190
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Uemori, T., Sato, Y., Fujita, T., Miyake, K., Mukai, H., Asada, K. and
            Kato, I.
TITLE      DNA polymerase-related factors
JOURNAL    Patent: US 6218150-A 67 17-APR-2001;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x ARI146001 (1-20)

Qy          156 GluArgThrPheLys 160
Db          3 GAGAGAACTTTCAG 17

RESULT 232
ARI153854/c
LOCUS       ARI153854          20 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6238624.
ACCESSION  ARI153854
VERSION    ARI153854.1  GI:15121907
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Klein, C.A., Murphy, A.J.M., Fowlkes, D.M., Broach, J., Manfredi, J.,
            Heller, M.J., Tu, E., Evans, G.A. and Sosnowski, R.G.
TITLE      Methods for transport in molecular biological analysis and
            diagnostics
JOURNAL    Patent: US 6238624-A 7 29-MAY-2001;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x ARI153854 (1-20)

Qy          56 HisValGluLeuLeu 60
Db          18 CACGTAGACTGCTC 4

RESULT 233
ARI160290/c
LOCUS       ARI160290          20 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 47 from patent US 6255059.
ACCESSION  ARI160290
VERSION    ARI160290.1  GI:16223938
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Klein, C.A., Murphy, A.J.M., Fowlkes, D.M., Broach, J., Manfredi, J.,
            Paul, J. and Trueheart, J.
TITLE      Methods for identifying G protein coupled receptor effectors
JOURNAL    Patent: US 6255059-A 47 03-JUL-2001;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x ARI160290 (1-20)

Qy          104 LeuSerLeuArgIle 108
Db          18 CTGAGTCTTCCATC 4

RESULT 234
ARI160292/c
LOCUS       ARI160292          20 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 49 from patent US 6255059.
ACCESSION  ARI160292
VERSION    ARI160292.1  GI:16223940
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Klein, C.A., Murphy, A.J.M., Fowlkes, D.M., Broach, J., Manfredi, J.,
```



Paul, J. and Trueheart, J.  
Methods for identifying G protein coupled receptor effectors  
JOURNAL Patent: US 625059-A 49 03-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR160292 (1-20)

QY 104 LeuSerLeuArgIle 108  
Db 18 CTGAGTCTTCGCATC 4

RESULT 235  
AR161622  
LOCUS Sequence 4 from patent US 6255475.  
DEFINITION AR161622  
ACCESSION AR161622  
VERSION AR161622.1 GI:16227596  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kwiatkowski, M.  
TITLE Chain terminators, the use thereof for nucleic acid sequencing and synthesis and a method of their preparation  
JOURNAL Patent: US 6255475-A 4 03-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR161622 (1-20)

QY 32 ValValLysArgArg 36  
Db 5 GTTGTAACACGACGG 19

RESULT 236  
AR162723  
LOCUS Sequence 45 from patent US 6258790.  
DEFINITION AR162723  
ACCESSION AR162723  
VERSION AR162723.1 GI:16230060  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett, C. Frank., Condon, T. P. and Cowser, L. M.  
TITLE Antisense modulation of integrin .alpha.4 expression  
JOURNAL Patent: US 6258790-A 45 10-JUL-2001;  
FEATURES Location/Qualifiers

Paul, J. and Trueheart, J.  
Methods for identifying G protein coupled receptor effectors  
JOURNAL Patent: US 625059-A 49 03-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR162723 (1-20)

QY 181 LeuProLeuTyrGlu 185  
Db 4 TTGCCCTTATATGAG 15

RESULT 237  
AR162748  
LOCUS Sequence 71 from patent US 6258790.  
DEFINITION AR162748  
ACCESSION AR162748  
VERSION AR162748.1 GI:16230086  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett, C. Frank., Condon, T. P. and Cowser, L. M.  
TITLE Antisense modulation of integrin .alpha.4 expression  
JOURNAL Patent: US 6258790-A 71 10-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR162748 (1-20)

QY 181 LeuProLeuTyrGlu 185  
Db 4 TTGCCCTTATATGAG 15

RESULT 238  
AR163037  
LOCUS Sequence 20 from patent US 6270963.  
DEFINITION AR163037  
ACCESSION AR163037  
VERSION AR163037.1 GI:16233512  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Stevens, J. K., Dunn, J. M., Capatos, D. and Matthews, D. E.  
TITLE Method for testing for mutations in DNA from a patient sample  
JOURNAL Patent: US 6270963-A 20 07-AUG-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

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Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR163037 (1-20)

QY 28 TyrLeuCystrVal 32 20 bp DNA linear PAT 17-OCT-2001
Db 2 TACCTATGTTATGTT 16

RESULT 239
AR163747
LOCUS AR163747 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 34 from patent US 6271029.
ACCESSION AR163747
VERSION AR163747.1 GI:16234455
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Cowse, L. M.
TITLE Antisense inhibition of cytohesin-2 expression
JOURNAL Patent: US 6271029-A 34 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR163747 (1-20)

QY 56 HisValGluLeu 60
Db 6 CATGTTGACTTCTT 20

RESULT 240
AR163777
LOCUS AR163777 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 64 from patent US 6271029.
ACCESSION AR163777
VERSION AR163777.1 GI:16234507
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Cowse, L. M.
TITLE Antisense inhibition of cytohesin-2 expression
JOURNAL Patent: US 6271029-A 64 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

US-09-966-880A-8 (1-198) x AR163037 (1-20)

QY 28 TyrLeuCystrVal 32 20 bp DNA linear PAT 17-OCT-2001
Db 2 TACCTATGTTATGTT 16

RESULT 239
AR163747
LOCUS AR163747 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 34 from patent US 6271029.
ACCESSION AR163747
VERSION AR163747.1 GI:16234455
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Cowse, L. M.
TITLE Antisense inhibition of cytohesin-2 expression
JOURNAL Patent: US 6271029-A 34 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR163747 (1-20)

QY 56 HisValGluLeu 60
Db 6 CATGTTGACTTCTT 20

RESULT 240
AR163777
LOCUS AR163777 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 64 from patent US 6271029.
ACCESSION AR163777
VERSION AR163777.1 GI:16234507
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Cowse, L. M.
TITLE Antisense inhibition of cytohesin-2 expression
JOURNAL Patent: US 6271029-A 64 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR170745 (1-20)

QY 172 LeuSerArgGlnLeu 176
Db 3 CTCCTCGCAGACGCTG 17

RESULT 242
AR170745
LOCUS AR170745 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 12 from patent US 6291741.
ACCESSION AR170745
VERSION AR170745.1 GI:17908704
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul, W., Scott, R. John., Betzner, A., Huttner, E., Lenee, P. and Perez, P.
TITLE Method for the production of modified plants
JOURNAL Patent: US 6291741-A 12 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR170745 (1-20)

```

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

RESULT 243  
LOCUS ARI170749 20 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 16 from patent US 6291741.  
ACCESSION ARI170749  
VERSION ARI170749.1 GI:17908708  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Paul W., Scott, R.John., Betzner, A., Huttner, E., Lensee, P. and Perez, P.  
TITLE Method for the production of modified plants  
JOURNAL Patent: US 6291741-A 16 18-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI170749 (1-20)

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

RESULT 244  
LOCUS ARI170751 20 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 18 from patent US 6291741.  
ACCESSION ARI170751  
VERSION ARI170751.1 GI:17908710  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Paul, W., Scott, R.John., Betzner, A., Huttner, E., Lensee, P. and Perez, P.  
TITLE Method for the production of modified plants  
JOURNAL Patent: US 6291741-A 18 18-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI170751 (1-20)

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

Db 2 GTTGTAACGACGG 16

RESULT 245  
LOCUS ARI173022/c 20 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 147 from patent US 6303374.  
ACCESSION ARI173022  
VERSION ARI173022.1 GI:17912513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Zhang, H. and Cowser, L.M.  
TITLE Antisense modulation of caspase 3 expression  
JOURNAL Patent: US 6303374-A 147 16-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI173022 (1-20)

Qy 41 SerPheSerLeuAsp 45  
Db 15 TCCTTCCTCCCTGGAC 1

RESULT 246  
LOCUS ARI173845 20 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 43 from patent US 6306606.  
ACCESSION ARI173845  
VERSION ARI173845.1 GI:17914165  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Weber, M.J., Wyatt, J. and Cowser, L.M.  
TITLE Antisense modulation of MP-1 expression  
JOURNAL Patent: US 6306606-A 43 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI173845 (1-20)

Qy 72 ProGlyArgCysTyr 76  
Db 2 CCTGTAGCTGTAT 15

RESULT 247  
LOCUS ARI178823 20 bp DNA linear PAT 20-APR-2002

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DEFINITION Sequence 69 from patent US 6319906.
ACCESSION ARI78823
VERSION ARI78823.1 GI:20219961
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6319906-A 69 20-NOV-2001;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x ARI78823 (1-20)
QY 176 LeuArgArgIleu 180
Db 1 CTGCGCGAATCCTG 15
RESULT 248
ARI78920
LOCUS ARI78920 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 166 from patent US 6319906.
ACCESSION ARI78920
VERSION ARI78920.1 GI:20220058
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6319906-A 166 20-NOV-2001;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x ARI78920 (1-20)
QY 176 LeuArgArgIleu 180
Db 2 CTGCGCGAATCCTG 16
RESULT 249
BD227783
LOCUS BD227783 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of integrin alph 4 expression.
ACCESSION BD227783
VERSION BD227783.1 GI:33037553
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Antisense modulation of integrin alph 4 expression
JOURNAL Patent: JP 2002526555-A 45 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526555-A/45
PF 19-AUG-1999 JP 2000574727
PI FRANK C BENNETT,THOMAS P CONDON,LEX M COWSBERT PC
C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
00,A61P1/16,
PC A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P29/00,A61P35/00, PC
A61P35/04,
PC A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
antisense sequence
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Artificial Sequence".
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x BD227783 (1-20)
QY 181 LeuProLeuTyGlu 185
Db 1 TTGCCTTATATGAG 15
RESULT 250
BD230169/c
LOCUS BD230169 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230169
VERSION BD230169.1 GI:33039939
KEYWORDS JP 2002530091-A/38.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Galibert,F. and Andre,C.
TITLE Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes
JOURNAL Patent: JP 2002530091-A 38 17-SEP-2002;
COMMENT OS Canis familiaris (dog)
PN JP 2002530091-A/38
PF 17-SEP-2002
PI 13-NOV-1999 JP 2000582596
PI FRANCIS GALIBERT,CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC Ren04F08
FH Key Location/Qualifiers
FT source 1..20

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FT /organism='Canis familiaris (dog)'.  
 source Location/Qualifiers

FEATURES  
 source 1..20  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9615"

## ORIGIN

Alignment Scores: 9.13e+03 Length: 20  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 6

US-09-966-880A-8 (1-198) x BD230169 (1-20)

QY 129 LeuHisArgAlaGly 133

DB 20 CTCACAGGCGAGGG 6

RESULT 251

BD237751/c

LOCUS

DEFINITION

Human proteins participating in protein decomposition of

endoplasmic reticulum.

ACCESSION

BD237751

VERSION

BD237751.1 GI:33047521

KEYWORDS

JP 2002527111-A/5.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 20)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CHAU V.

HUMAN PROTEINS PARTICIPATING IN PROTEIN DECOMPOSITION OF

ENDOPLASMIC RETICULUM

PATENT: JP 2002527111-A 5 27-AUG-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002527111-A/5

PD 27-AUG-2002

PF 21-OCT-1999 JP 2000577306

PR 21-OCT-1998 US 60/105064

PI VINCENT CHAU

PC C12N15/09,A61K31/7105,A61K45/00,A61K48/00,A61P1/16,A61P11/00,

PC A61P35/00,C12N9/00,C12Q1/02,C12Q1/68,C12N15/00 CC Human

PC C07K14/47,C12N9/00,C12Q1/02,C12Q1/68,C12N15/00 CC Human

proteins participating in protein decomposition of CC

endoplasmic

reticulum

CC reticulum

FT Key

FT source

FT Location/Qualifiers

1..20

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 9.13e+03 Length: 20

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD237751 (1-20)

QY 130 HisArgAlaGlyVal 134

Db

RESULT 252

E07640

LOCUS

DEFINITION

Oligonucleotide.

ACCESSION

E07640

VERSION

E07640.1 GI:2175775

KEYWORDS

JP 1994153997-A/1.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 20)

Okamoto,H., Yamamoto,N., Tomita,Y., Kawaguchi,M., Murakami,A. and

Makino,K.

METHOD FOR DETECTING TARGET NUCLEIC ACID BY AMPLIFICATION OF

DETECTED SIGNAL

PATENT: JP 1994153997-A 1 03-JUN-1994;

CANON INC

OS None

OC Artificial sequences.

PN JP 1994153997-A/1

PD 03-JUN-1994

PF 27-NOV-1992 JP 1992318958

PI OKAMOTO HISASHI, YAMAMOTO NOBUKO, TOMITA YOSHINORI, PI

KAWAGUCHI MASAHIRO,

PI MURAKAMI AKIRA, MAKINO KEISUKE

PC C12Q1/68,C07H21/04,G01N24/00,G01N33/58//A61B10/00; CC

strandedness: Single;

CC topology: Linear;

FT Key

FT Location/Qualifiers

1..20

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FEATURES

source

1..20

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 9.13e+03 Length: 20

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x E07640 (1-20)

QY 32 ValVallyLysArgArg 36

DB 1 GTTGTAACACGCG 15

RESULT 253

E07641

LOCUS

DEFINITION

Oligonucleotide.

ACCESSION

E07641

VERSION

E07641.1 GI:2175776

KEYWORDS

JP 1994153998-A/1.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 20)

Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y., Makino,K. and

Murakami,A.

METHOD FOR DETECTING NUCLEIC ACID HYBRID BODY AND PROBE USED

PATENT: JP 1994153998-A 1 03-JUN-1994;

CANON INC

OS None

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OC Artificial sequences.
PN JP 1994153998-A/1
PD 03-JUN-1994
PF 27-NOV-1992 JP 1992318959
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASASHIRO, PI
TOMITA YOSHINORI,
PI MAKINO KEISUKE, MURAKAMI AKIRA
PC C12Q1/68, C07H21/04, G01N24/00, G01N33/58//A61B10/00; CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT source /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..20
/db_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E07641 (1-20)
QY 32 ValVallysArgArg 36
DB 1 GTTGTAAACGACGG 15
RESULT 254
E07642
LOCUS E07642 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide.
ACCESSION E07642
VERSION E07642.1 GI:2175777
KEYWORDS JP 1994153998-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y., Makino,K. and
Murakami,A.
TITLE METHOD FOR DETECTING TARGET NUCLEIC ACID USING CHARGE TRANSFER TYPE
PIGMENT AND PROBE USED THEREFOR
JOURNAL Patent: JP 1994153998-A 1 03-JUN-1994;
CANON INC
COMMENT OS None
OC Artificial sequences.
PN JP 1994153999-A/1
PD 03-JUN-1994
PF 30-NOV-1992 JP 1992320500
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASASHIRO, PI
TOMITA YOSHINORI,
PI MAKINO KEISUKE, MURAKAMI AKIRA
PC C12Q1/68, C07H21/04, G01N21/17, G01N24/00, G01N33/58//A61B10/00;
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT source /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..20
/db_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E07641 (1-20)
QY 32 ValVallysArgArg 36
DB 1 GTTGTAAACGACGG 15
RESULT 254
E07642
LOCUS E07642 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide.
ACCESSION E07642
VERSION E07642.1 GI:2175777
KEYWORDS JP 1994153998-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y., Makino,K. and
Murakami,A.
TITLE METHOD FOR DETECTING TARGET NUCLEIC ACID USING CHARGE TRANSFER TYPE
PIGMENT AND PROBE USED THEREFOR
JOURNAL Patent: JP 1994153998-A 1 03-JUN-1994;
CANON INC
COMMENT OS None
OC Artificial sequences.
PN JP 1994153999-A/1
PD 03-JUN-1994
PF 30-NOV-1992 JP 1992320500
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASASHIRO, PI
TOMITA YOSHINORI,
PI MAKINO KEISUKE, MURAKAMI AKIRA
PC C12Q1/68, C07H21/04, G01N21/17, G01N24/00, G01N33/58//A61B10/00;
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT source /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..20
/db_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E07642 (1-20)
QY 32 ValVallysArgArg 36
DB 1 GTTGTAAACGACGG 15
RESULT 255
E10364
LOCUS E10364 20 bp DNA linear PAT 29-SEP-1997
DEFINITION M13mpl8DNA probe.
ACCESSION E10364
VERSION E10364.1 GI:22027193
KEYWORDS JP 1995313199-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N. and Okamoto,H.
TITLE DETECTION OF TARGET SUBSTANCE IN SPECIMEN
JOURNAL Patent: JP 1995313199-A 1 05-DEC-1995;
CANON INC
COMMENT OS None
OC Artificial sequences.
PN JP 1995313199-A/1
PD 05-DEC-1995
PF 26-MAY-1994 JP 1994112626
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI
PC C12Q1/68, G01N33/58//C07D309/34, C07D335/02, C07D409/04, PC
C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT source /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E10364 (1-20)
QY 32 ValVallysArgArg 36
DB 1 GTTGTAAACGACGG 15
RESULT 256
E12624
LOCUS E12624 20 bp DNA linear PAT 27-APR-1998
DEFINITION DNA probe.
ACCESSION E12624
VERSION E12624.1 GI:3251456
KEYWORDS JP 1997040661-A/1.
SOURCE unclassified

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ORGANISM      unidentified
unclassified.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y. and Miyazaki,I.
TITLE        FLUORESCENT DYE CONTAINING PYRYLIUM SALT OR PYRYLIUM ANALOGOUS
              SALT, AND DETECTION OF NUCLEIC ACID AND FLUORESCENT DYEING OF
              ORGANISM SPECIMEN USING THE SAME
JOURNAL       Patent: JP 1997040661-A 1 10-FEB-1997;
              CANON INC
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1997040661-A/1
              PD 10-FEB-1997
              PF 17-DEC-1993 JP 1996200327
              PR 21-DEC-1992 JP 92P 340755, 10-MAR-1993 JP 93P 49530, PR
              13-SEP-1993 JP 93P 227204, 26-OCT-1993 JP 93P 266866 PI
              YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASAHIRO, PI
              YOSHINORI,
              PI MIYAZAKI TAKESHI
              PC C07D309/34;C07D335/02,C07D345/00,C09K11/06,C12Q1/68,G01N21/78,
              PC G01N27/447,
              PC G01N33/50//C07D407/14,C07D409/08,C07D409/14,C12N15/09; CC
              strandedness: single;
              CC Topology: Linear;
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Artificial sequences'.
FEATURES      source
              Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E12624 (1-20)
QY 32 ValVallysArgArg 36
Db 1 GTTGTAACGACGG 15
RESULT 257
E25557 20 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION Method for detecting target nucleic acid.
ACCESSION E25557
VERSION E25557.1 GI:13024823
KEYWORDS JP 1999127862-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE Method for detecting target nucleic acid
JOURNAL Patent: JP 1999127862-A 1 18-MAY-1999;
              CANON INC
COMMENT OS Unidentified
              PN JP 1999127862-A/1
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300943
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              PC C12N15/09,C12Q1/68,C12N15/00
              CC Topology: Linear;
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.
FEATURES      source
              Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E25557 (1-20)
QY 32 ValVallysArgArg 36
Db 1 GTTGTAACGACGG 15
RESULT 258
E25563 20 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION Method for detecting target nucleic acid.
ACCESSION E25563
VERSION E25563.1 GI:13024829
KEYWORDS JP 1999127897-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE Method for detecting target nucleic acid
JOURNAL Patent: JP 1999127897-A 1 18-MAY-1999;
              CANON INC
COMMENT OS Unidentified
              PN JP 1999127897-A/1
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              PC C12Q1/68//C12N15/09,C12N15/00
              CC Topology: Linear;
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.
FEATURES      source
              Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x E25563 (1-20)
QY 32 ValVallysArgArg 36
Db 1 GTTGTAACGACGG 15
RESULT 259

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E25564/c
LOCUS          E25564          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25564
VERSION        E25564.1  GI:13024830
KEYWORDS       JP 199127897-A/2.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE          Method for detecting target nucleic acid
JOURNAL        Patent: JP 199127897-A 2 18-MAY-1999;
               CANON INC
COMMENT        OS Unidentified
               PN JP 1999127897-A/2
               PD 18-MAY-1999
               PF 31-OCT-1997 JP 1997300944
               PR
               PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
               MITSUHIKO SHIOYA
               PC C12Q1/68//C12N15/09,C12N15/00
               CC Topology: Linear;
               FH Key Location/Qualifiers
               FT source 1..20
               FT /organism='Unidentified'.

FEATURES       Location/Qualifiers
               source 1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25564 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25568          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25568
VERSION        E25568.1  GI:13024834
KEYWORDS       JP 199127897-A/6.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE          Method for detecting target nucleic acid
JOURNAL        Patent: JP 199127897-A 6 18-MAY-1999;
               CANON INC
COMMENT        OS Unidentified
               PN JP 1999127897-A/6
               PD 18-MAY-1999
               PF 31-OCT-1997 JP 1997300944
               PR
               PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
               MITSUHIKO SHIOYA
               PC C12Q1/68//C12N15/09,C12N15/00
               CC Topology: Linear;
               FH Key Location/Qualifiers
               FT source 1..20
               FT /organism='Unidentified'.

FEATURES       Location/Qualifiers
               source 1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25564 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25567/c          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25567
VERSION        E25567.1  GI:13024833
KEYWORDS       JP 199127897-A/5.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE          Method for detecting target nucleic acid
JOURNAL        Patent: JP 199127897-A 5 18-MAY-1999;
               CANON INC
COMMENT        OS Unidentified
               PN JP 1999127897-A/5
               PD 18-MAY-1999
               PF 31-OCT-1997 JP 1997300944
               PR
               PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
               MITSUHIKO SHIOYA
               PC C12Q1/68//C12N15/09,C12N15/00
               CC Topology: Linear;
               FH Key Location/Qualifiers
               FT source 1..20
               FT /organism='Unidentified'.

FEATURES       Location/Qualifiers
               source 1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25567/c          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25567
VERSION        E25567.1  GI:13024833
KEYWORDS       JP 199127897-A/5.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE          Method for detecting target nucleic acid
JOURNAL        Patent: JP 199127897-A 5 18-MAY-1999;
               CANON INC
COMMENT        OS Unidentified
               PN JP 1999127897-A/5
               PD 18-MAY-1999
               PF 31-OCT-1997 JP 1997300944
               PR
               PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
               MITSUHIKO SHIOYA
               PC C12Q1/68//C12N15/09,C12N15/00
               CC Topology: Linear;
               FH Key Location/Qualifiers
               FT source 1..20
               FT /organism='Unidentified'.

FEATURES       Location/Qualifiers
               source 1..20
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               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 262
E36214
LOCUS          E36214          20 bp      DNA          linear          PAT 31-JAN-2002

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FT
FEATURES       Location/Qualifiers
               source 1..20
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               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 261
LOCUS          E25568          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25568
VERSION        E25568.1  GI:13024834
KEYWORDS       JP 199127897-A/6.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE          Method for detecting target nucleic acid
JOURNAL        Patent: JP 199127897-A 6 18-MAY-1999;
               CANON INC
COMMENT        OS Unidentified
               PN JP 1999127897-A/6
               PD 18-MAY-1999
               PF 31-OCT-1997 JP 1997300944
               PR
               PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
               MITSUHIKO SHIOYA
               PC C12Q1/68//C12N15/09,C12N15/00
               CC Topology: Linear;
               FH Key Location/Qualifiers
               FT source 1..20
               FT /organism='Unidentified'.

FEATURES       Location/Qualifiers
               source 1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:       0

US-09-966-880A-8 (1-198) x E25568 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 262
E36214
LOCUS          E36214          20 bp      DNA          linear          PAT 31-JAN-2002

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```

DEFINITION Japanese citrus viroid 1 (JCVd1) gene.
ACCESSION E36214
VERSION E36214.1 GI:18626426
KEYWORDS JP 2000166566-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ito,T., Yoshiro,H. and Ozaki,K.
TITLE Japanese citrus viroid 1 (JCVd1) gene
JOURNAL Patent: JP 2000166566-A 6 20-JUN-2000;
FRUIT TREE RES STATION
OS Artificial Sequence
PN JP 2000166566-A/6
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349471
PR
PI TAKAO ITO,HIROYUKI YASHIRO,KATSUMI OZAKI
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E59388 (1-20)
QY 40 ThrSerPheSerLeu 44
DB 1 ACCTCGTTTAGTTG 15
RESULT 264
E64279
LOCUS 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Polynucleotide molecule encoding Neospora protein.
ACCESSION E64279
VERSION E64279.1 GI:13017785
KEYWORDS JP 1999332583-A/11.
SOURCE Neospora caninum
ORGANISM Neospora caninum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Neospora.
REFERENCE 1 (bases 1 to 20)
AUTHORS David,A.B., Rebecca,A.M., Bekki,A.D., Barakurishunan,R.K. and
Susan,C.Y.
TITLE Polynucleotide molecule encoding Neospora protein
JOURNAL Patent: JP 1999332583-A 11 07-DEC-1999;
Pfizer Prod Inc
COMMENT OS Neospora caninum
PN JP 1999332583-A/11
PD 07-DEC-1999
PF 25-MAR-1999 JP 1999081833
PR 26-MAR-1998 US 60/079389,15-DEC-1998 US 60/112282 PI
DAVID ALLAN BLAKE,REBECCA ANNE MADURA,BEKKI ANNE DATSUKI, PI
BARAKURISHUNAN RAJENDORA KRISHNAN,SUSAN CHRISTINE YODA PC
C12N15/09,A61K31/00,A61K35/12,A61K38/00,A61K39/39,C07K14/44, PC
C07K16/18,
PC C12N15/02,C12P21/02,C12P21/08,C12N15/00,A61K37/02,C12N15/00 CC
FEATURES
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Neospora caninum'.
FEATURES
source Location/Qualifiers
1..20
/organism='Neospora caninum'
/mol_type='genomic DNA'
/db_xref='taxon:29176'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E64279 (1-20)
QY 39 AlaThrSerPheSer 43
DB 4 GCGACTCTCTTTCT 18
DEFINITION Japanese citrus viroid 1 (JCVd1) gene.
ACCESSION E36214
VERSION E36214.1 GI:18626426
KEYWORDS JP 2000166566-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ito,T., Yoshiro,H. and Ozaki,K.
TITLE Japanese citrus viroid 1 (JCVd1) gene
JOURNAL Patent: JP 2000166566-A 6 20-JUN-2000;
FRUIT TREE RES STATION
OS Artificial Sequence
PN JP 2000166566-A/6
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349471
PR
PI TAKAO ITO,HIROYUKI YASHIRO,KATSUMI OZAKI
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E36214 (1-20)
QY 97 PheLeuArgGlyAsn 101
DB 5 TTCTCCGGGGAAC 19
RESULT 263
E59388
LOCUS 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for differentiating varieties of pig by DNA sequence
polymorphism.
ACCESSION E59388
VERSION E59388.1 GI:18622523
KEYWORDS JP 200030586-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mitsuhashi,T. and Okumura,N.
TITLE Method for differentiating varieties of pig by DNA sequence
JOURNAL Patent: JP 200030586-A 12 19-DEC-2000;
LIVESTOCK EXPERIMENT STATION MINISTRY OF AGRICULTURE FORESTRY AND
FISHERIES, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY
AND FISHERIES, TADAYOSHI MITSUHASHI
OS Artificial Sequence
PN JP 200030586-A/12
PD 19-DEC-2000
PF 11-JUN-1999 JP 1999165269
PR
PI TADAYOSHI MITSUHASHI,NAOHIKO OKUMURA
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.

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RESULT 265
I16233
LOCUS I16233 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 59 from patent US 5475096.
ACCESSION I16233
VERSION I16233.1 GI:1251141
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gold,L. and Tuerk,C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5475096-A 59 12-DEC-1995;
FEATURES
    source
        Location/Qualifiers
            1..20
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ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I16233 (1-20)
QY 32 ValVallysArgArg 36
DB 4 GTTGTAACGACGG 18
RESULT 266
I23911/c
LOCUS I23911 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5541060.
ACCESSION I23911
VERSION I23911.1 GI:1603781
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bell,G.I., Stoffel,M., Takeda,J., Vionnet,N., Yasuda,K.,
Pikis,S.J., Zouali,H., Velho,G., Cohen,D. and Froguel,P.
TITLE Detection of glucokinase-linked early-onset non-insulin-dependent
diabetes mellitus
JOURNAL Patent: US 5541060-A 13 30-JUL-1996;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I23911 (1-20)
QY 104 LeuSerLeuArgIle 108
DB 18 TTGACCTCAGAATC 4
RESULT 267
I24636
LOCUS I24636 20 bp DNA linear PAT 07-OCT-1996

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DEFINITION Sequence 20 from patent US 5545527.
ACCESSION I24636
VERSION I24636.1 GI:1604506
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Stevens,J.K. and Dunn,J.M.
TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 5545527-A 20 13-AUG-1996;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I24636 (1-20)
QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTTATGTT 16
RESULT 268
I25233
LOCUS I25233 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 20 from patent US 5550020.
ACCESSION I25233
VERSION I25233.1 GI:1605103
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for
retinoblastoma
JOURNAL Patent: US 5550020-A 20 27-AUG-1996;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I25233 (1-20)
QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTTATGTT 16
RESULT 269
I31646
LOCUS I31646 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 47 from patent US 5582983.
ACCESSION I31646
VERSION I31646.1 GI:1822437
KEYWORDS

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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Anderson,D.M. and Scholin,C.A.  
TITLE Genetic markers and methods of identifying alexandrium  
(dinophyceae) species  
JOURNAL Patent: US 5582983-A 47 10-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x I31646 (1-20)  
Qy 170 ValArgLeuSerArg 174  
Db 6 GTCGCTCTTCAGA 20  
RESULT 270  
I36171/c 136171 20 bp DNA linear PAT 13-MAY-1997  
LOCUS Sequence 7 from patent US 5605662.  
DEFINITION I36171  
ACCESSION I36171.1 GI:2086684  
VERSION I36171.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Heller,M.J. and Tu,E.  
TITLE Active programmable electronic devices for molecular biological  
analysis and diagnostics  
JOURNAL Patent: US 5605662-A 7 25-FEB-1997;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x I36171 (1-20)  
Qy 56 HisValGluLeuLeu 60  
Db 18 CACGTAGAACTGCTC 4  
RESULT 271  
I36258  
LOCUS Sequence 3 from patent US 5605797.  
DEFINITION I36258  
ACCESSION I36258  
VERSION I36258.1 GI:2086771  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.  
TITLE Bovine .beta.-mannosidase gene and methods of use  
JOURNAL Patent: US 5605797-A 3 25-FEB-1997;  
FEATURES Location/Qualifiers  
source 1..20  
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/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x I36258 (1-20)  
Qy 179 IleLeuLeuProLeu 183  
Db 6 ATTCCTTTACCCCTG 20  
RESULT 272  
I41050  
LOCUS Sequence 1 from patent US 5624798.  
DEFINITION I41050  
ACCESSION I41050.1 GI:2081640  
VERSION I41050.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Yamamoto,N., Okamoto,T., Tomida,Y., Miyazaki,T. and Kawaguchi,M.  
TITLE Detection method of nucleic acid by use of fluorescent pyrylium  
stain in intercalation into nucleic acids  
JOURNAL Patent: US 5624798-A 1 29-APR-1997;  
FEATURES Location/Qualifiers  
source 1..20  
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/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x I41050 (1-20)  
Qy 32 ValVallylsArgArg 36  
Db 1 GTTGTAAACGACGG 15  
RESULT 273  
I66719  
LOCUS Sequence 59 from patent US 5670637.  
DEFINITION I66719  
ACCESSION I66719.1 GI:2724697  
VERSION I66719.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Gold,L. and Tuerk,C.  
TITLE Nucleic acid ligands  
JOURNAL Patent: US 5670637-A 59 23-SEP-1997;

[illegible]

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
DB: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x I84813 (1-20)

QY 32 ValVallysargarg 36  
DB 4 GTTGTAAACGACGG 18  
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RESULT 278

AR180892 AR180892 20 bp DNA linear PAT 20-APR-2002

LOCUS Definition Sequence 67 from patent US 6333158.

ACCESSION AR180892

VERSION AR180892.1 GI:20222925

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Uemori, T., Sato, Y., Fujita, T., Miyake, K., Mukai, H., Asada, K. and

Kato, I.

TITLE DNA polymerase-related factors

JOURNAL Patent: US 6333158-A 67 25-DEC-2001;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
DB: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x AR180892 (1-20)

QY 156 GluArgThrPheLys 160  
DB 3 GAGAGACTTTCAG 17  
|||||

RESULT 279

AR216046 AR216046 20 bp DNA linear PAT 25-SEP-2002

LOCUS Definition Sequence 93 from patent US 6410518.

ACCESSION AR216046

VERSION AR216046.1 GI:23314334

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Monia, B.P.

TITLE Antisense oligonucleotide inhibition of raf gene expression

JOURNAL Patent: US 6410518-A 93 25-JUN-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
DB: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x AR216046 (1-20)

QY 169 SerValArgLeuSer 173  
DB 4 TCTGTAAAGGCTTCA 18  
|||||

RESULT 280

AR224743 AR224743 20 bp DNA linear PAT 26-SEP-2002

LOCUS Definition Sequence 48 from patent US 6440739.

ACCESSION AR224743

VERSION AR224743.1 GI:23333583

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett, C.F. and Freier, S.M.

TITLE Antisense modulation of glioma-associated oncogene-2 expression

JOURNAL Patent: US 6440739-A 48 27-AUG-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
DB: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x AR224743 (1-20)

QY 130 HisArgAlaGlyVal 134  
DB 20 CACCGGCAGGTGTA 6  
|||||

RESULT 281

AR225942 AR225942 20 bp DNA linear PAT 20-DEC-2002

LOCUS Definition Sequence 5 from patent US 6444465.

ACCESSION AR225942

VERSION AR225942.1 GI:27264096

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wyatt, J. and Freier, S.M.

TITLE Antisense modulation of Her-1 expression

JOURNAL Patent: US 6444465-A 5 03-SEP-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
DB: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x AR225942 (1-20)

QY 129 LeuHisArgAlaGly 133  
|||||

Db 6 TTGCACAGGCGAGGG 20  
RESULT 282  
AR229992  
LOCUS 20 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 35 from patent US 6451538.  
ACCESSION AR229992  
VERSION AR229992.1 GI:27269884  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Cowser,L.M.  
TITLE Antisense modulation of CHK2 expression  
JOURNAL Patent: US 6451538-A 35 17-SEP-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.13e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR229992 (1-20)  
QY 110 ThrAlaArgLeuTyr 114  
Db 4 ACAGCAGCGTTATAC 18  
RESULT 283  
AR232363  
LOCUS 20 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 58 from patent US 6455308.  
ACCESSION AR232363  
VERSION AR232363.1 GI:27274355  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Freier,S.M.  
TITLE Antisense modulation of serum amyloid A4 expression  
JOURNAL Patent: US 6455308-A 58 24-SEP-2002;  
FEATURES Location/Qualifiers  
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QY 42 PheSerLeuAppPhe 46  
Db 3 TTCCTGTTGGACTTC 17  
RESULT 284  
AR234630/c  
LOCUS 20 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 71 from patent US 6458591.  
ACCESSION AR234630  
VERSION AR234630.1 GI:27277337  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Wyatt,J.  
TITLE Antisense modulation of phosphorylase kinase Alpha 2 expression  
JOURNAL Patent: US 6458591-A 71 01-OCT-2002;  
FEATURES Location/Qualifiers  
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QY 38 SerAlaThrSerPhe 42  
Db 15 TCTGCCACTTCTTTT 1  
RESULT 285  
AR255289  
LOCUS 20 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 56 from patent US 6482592.  
ACCESSION AR255289  
VERSION AR255289.1 GI:27304338  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Lundeberg,J. and Uhlen,M.  
TITLE Methods and kits for isolating primer extension products using modular oligonucleotides  
JOURNAL Patent: US 6482592-A 56 19-NOV-2002;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x AR255289 (1-20)  
QY 32 ValVallylsArgArg 36  
Db 2 GTTGTAAACGACGG 16  
RESULT 286  
AR263237  
LOCUS 20 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 59 from patent US 6331398.  
ACCESSION AR263237  
VERSION AR263237.1 GI:28074982  
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Gold,L. and Tuerk,C.
TITLE        Nucleic acid ligands
JOURNAL      Patent: US 6313198-A 59 18-DEC-2001;
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Percent Similarity: 100.00%    Conservative: 0
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DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AR263237 (1-20)

QY          32 ValVallylsArgArg 36
Db          4 GTTGTAACGACGG 18

RESULT 287
LOCUS       AR272008                20 bp    DNA    linear    PAT 10-APR-2003
DEFINITION  Sequence 78 from patent US 6503756.
ACCESSION   AR272008
VERSION     AR272008.1 GI:29703576
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Freier,S.M. and Wyatt,J.
TITLE        Antisense modulation of syntaxin 4 interacting protein expression
JOURNAL      Patent: US 6503756-A 78 07-JAN-2003;
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              source
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Best Local Similarity: 100.00% Mismatches:      0
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US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY          44 LeuAspPheGlyTyr 48
Db          17 CTGGACTTGGGTAT 3

RESULT 288
LOCUS       AR312669/C              20 bp    DNA    linear    PAT 12-JUN-2003
DEFINITION  Sequence 3206 from patent US 6559294.
ACCESSION   AR312669
VERSION     AR312669.1 GI:31706095
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3731 06-MAY-2003;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3731 06-MAY-2003;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3206 06-MAY-2003;
FEATURES     Location/Qualifiers
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Score:          5.00          Matches:      5
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Best Local Similarity: 100.00% Mismatches:      0
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DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AR312669 (1-20)

QY          103 AsnLeuSerLeuArg 107
Db          20 AACCTCTCTCTGAGG 6

RESULT 290
LOCUS       AR313194/C              20 bp    DNA    linear    PAT 12-JUN-2003
DEFINITION  Sequence 3731 from patent US 6559294.
ACCESSION   AR313194
VERSION     AR313194.1 GI:31706620
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3731 06-MAY-2003;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3704 06-MAY-2003;
FEATURES     Location/Qualifiers
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Pred. No.:      9.13e+03      Length:      20
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Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
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DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AR313167 (1-20)

QY          169 SerValArgLeuSer 173
Db          19 TCCGTGAGACTGTCT 5

RESULT 289
LOCUS       AR313167/C              20 bp    DNA    linear    PAT 12-JUN-2003
DEFINITION  Sequence 3704 from patent US 6559294.
ACCESSION   AR313167
VERSION     AR313167.1 GI:31706593
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3704 06-MAY-2003;
FEATURES     Location/Qualifiers
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ORIGIN
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Pred. No.:      9.13e+03      Length:      20
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Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6             Gaps:          0

US-09-966-880A-8 (1-198) x AR313167 (1-20)

QY          103 AsnLeuSerLeuArg 107
Db          20 AACCTCTCTCTGAGG 6

RESULT 290
LOCUS       AR313194/C              20 bp    DNA    linear    PAT 12-JUN-2003
DEFINITION  Sequence 3731 from patent US 6559294.
ACCESSION   AR313194
VERSION     AR313194.1 GI:31706620
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3731 06-MAY-2003;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
              Sankaran,B. and Fletcher,L.D.
TITLE        Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 3731 06-MAY-2003;
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Alignment Scores:
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DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR314123 (1-20)

QY 40 ThrSerPheSerLeu 44
DB 18 ACATCGTCTCCGCTA 4

RESULT 295
LOCUS AR314875 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5412 from patent US 6559294.
ACCESSION AR314875
VERSION AR314875.1 GI:31708301
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5412 06-MAY-2003;
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Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR314875 (1-20)

QY 126 LeuArgArgLeuHis 130
DB 17 CTAAGGCGCTTACAT 3

RESULT 296
LOCUS AR315172 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5709 from patent US 6559294.
ACCESSION AR315172
VERSION AR315172.1 GI:31708598
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5709 06-MAY-2003;
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AR315172 (1-20)

QY 104 LeuSerLeuArgile 108
DB 15 CTGTCTCTCCGCTA 1

RESULT 297
LOCUS AR315845 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6382 from patent US 6559294.
ACCESSION AR315845
VERSION AR315845.1 GI:31709271
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6382 06-MAY-2003;
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US-09-966-880A-8 (1-198) x AR315845 (1-20)

QY 58 GluLeuLeuPheLeu 62
DB 20 GAGCTTCTCTTTTA 6

RESULT 298
LOCUS AR315964 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6501 from patent US 6559294.
ACCESSION AR315964
VERSION AR315964.1 GI:31709390
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6501 06-MAY-2003;
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DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR315964 (1-20)

Qy 41 SerPheSerLeuasp 45

Db 5 AGTTTCTCTAGAC 19

RESULT 299

AR336993

LOCUS AR336993 20 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 54 from patent US 6566132.

ACCESSION AR336993

VERSION AR336993.1 GI:33722847

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Watt,A.T.

TITLE Antisense modulation of Interferon gamma receptor 1 expression

JOURNAL Patent: US 6566132-A 54 20-MAY-2003;

FEATURES

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Location/Qualifiers

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US-09-966-880A-8 (1-198) x AR336993 (1-20)

Qy 167 GluAsnSerValArg 171

Db 5 GAGAAATTCAGTGAGG 19

RESULT 300

AR350293/c

LOCUS AR350293 20 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 70 from patent US 6586245.

ACCESSION AR350293

VERSION AR350293.1 GI:33751264

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.F., Baker,B.F., Wyatt,J. and Davis,S.E.

TITLE Antisense modulation of CD40 ligand expression

JOURNAL Patent: US 6586245-A 70 01-JUL-2003;

FEATURES

source

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Location/Qualifiers

/organism="unknown"

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Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR350293 (1-20)

Qy 2 AspSerLeuLeuMet 6

Db 15 GACAGTCTTCTCATG 1

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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# SUMMARIES

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## ALIGNMENTS

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; Publication No. US2004005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 11764  
; LENGTH: 18  
; TYPE: DNA

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4	3.0	21	15	US-10-289-762-5376	Sequence 5376, Ap
5	2.5	13	10	US-09-877-478-6121	Sequence 6121, Ap
6	2.5	15	15	US-10-317-444-325	Sequence 325, App
7	2.5	15	15	US-10-317-444-326	Sequence 326, App
8	2.5	15	15	US-10-317-444-479	Sequence 479, App
9	2.5	15	15	US-10-317-444-480	Sequence 480, App
10	2.5	16	9	US-09-873-075A-4	Sequence 4, Appli
11	2.5	16	9	US-09-781-988-101	Sequence 101, App
12	2.5	16	10	US-09-771-933-189	Sequence 189, App
13	2.5	16	10	US-09-893-878-101	Sequence 101, App
14	2.5	16	11	US-09-896-095-101	Sequence 101, App
15	2.5	16	15	US-10-126-685-101	Sequence 101, App
16	2.5	16	15	US-10-127-028-101	Sequence 101, App
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18	2.5	17	9	US-09-866-108-9581	Sequence 9581, Ap
19	2.5	17	9	US-09-866-108-9582	Sequence 9582, Ap
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22	2.5	17	9	US-09-866-108-9631	Sequence 9631, Ap
23	2.5	17	9	US-09-866-108-9632	Sequence 9632, Ap
24	2.5	17	9	US-09-866-108-9765	Sequence 9765, Ap
25	2.5	17	9	US-09-866-108-9766	Sequence 9766, Ap
26	2.5	17	9	US-09-866-108-9767	Sequence 9767, Ap
27	2.5	17	10	US-09-825-803-345	Sequence 345, App
28	2.5	17	10	US-09-730-289B-634	Sequence 634, App
29	2.5	17	10	US-09-818-875-1415	Sequence 1415, Ap
30	2.5	17	10	US-09-818-875-1416	Sequence 1416, Ap
31	2.5	17	10	US-09-818-875-3818	Sequence 3818, Ap
32	2.5	17	10	US-09-818-875-3819	Sequence 3819, Ap
33	2.5	17	10	US-09-780-533A-382	Sequence 382, App
34	2.5	17	10	US-09-780-533A-1219	Sequence 1219, Ap
35	2.5	17	10	US-09-780-533A-1263	Sequence 1263, Ap
36	2.5	17	10	US-09-780-533A-1373	Sequence 1373, Ap
37	2.5	17	10	US-09-780-533A-1374	Sequence 1374, Ap
38	2.5	17	10	US-09-780-533A-2240	Sequence 2240, Ap
39	2.5	17	10	US-09-780-533A-2555	Sequence 2555, Ap
40	2.5	17	10	US-09-877-478-280	Sequence 280, App
41	2.5	17	10	US-09-877-478-373	Sequence 373, App
42	2.5	17	10	US-09-877-478-374	Sequence 374, App
43	2.5	17	10	US-09-877-478-1106	Sequence 1106, Ap
44	2.5	17	10	US-09-877-478-1486	Sequence 1486, Ap
45	2.5	17	10	US-09-848-754A-967	Sequence 967, App

```

; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3959, in complement
US-10-349-143-11764

Alignment Scores:
Pred. No.: 339 Length: 18
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-11764 (1-18)

QY 179 llsleuLeuProLeuTyr 184
Db 1 ATCCTTCTCCACTCTAC 18

RESULT 2
US-10-349-143-7618/c
; Sequence 7618, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.0200CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-04-22, 978
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7618
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-9709 for SEQ 3684,
US-10-349-143-7618

Alignment Scores:
Pred. No.: 357 Length: 19
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-7618 (1-19)

QY 167 GluBanserValArgLeu 172
Db 19 GAAATAGTGTAGGCTC 2

RESULT 3
US-10-349-143-9310
; Sequence 9310, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta

```

```

; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.0200CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-24508 for SEQ 1445, in compl
US-10-349-143-9310

Alignment Scores:
Pred. No.: 374 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-9310 (1-20)

QY 40 ThrSerPheSerLeuAsp 45
Db 2 ACAGTTCTCATTAGAC 19

RESULT 4
US-10-289-762-5376
; Sequence 5376, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5376
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5376

Alignment Scores:
Pred. No.: 374 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-5376 (1-20)

QY 167 GluBanserValArgLeu 172
Db 1 GAGAACTCGTGGCGCTG 18

RESULT 5
US-09-877-478-6121

```

```

; Sequence 6121, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6121
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6121

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-6121 (1-15)

QY 172 LeuSerArgGlnIeu 176
Db 1 CUUUCUGGCAACUU 15

RESULT 6
US-10-317-444-325
; Sequence 325, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12
US-10-317-444-325

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-325 (1-15)

QY 72 ProGlyArgCysTyr 76
Db 15 CCTGGACGGTGCTAC 15

RESULT 7
US-10-317-444-326/c
; Sequence 326, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12
US-10-317-444-326

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-326 (1-15)

QY 72 ProGlyArgCysTyr 76
Db 15 CCTGGACGGTGCTAC 15

RESULT 8
US-10-317-444-479
; Sequence 479, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7
US-10-317-444-479

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-479 (1-15)

QY 72 ProGlyArgCysTyr 76  
|||||  
DB 1 CCTGGACGGTGCTAC 15

RESULT 9  
US-10-317-444-480/C  
; Sequence 480, Application US/10317444  
; Publication No. US20030235837A1  
; GENERAL INFORMATION:  
; APPLICANT: Keim, Paul  
; APPLICANT: Keys, Christine  
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli  
; FILE REFERENCE: NAU2020US  
; CURRENT APPLICATION NUMBER: US/10/317,444  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: US 60/339,687  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 480  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Escherichia coli O157:H7  
US-10-317-444-480

Alignment Scores:  
Pred. No.: 3.29e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-480 (1-15)

QY 72 ProGlyArgCysTyr 76  
|||||  
DB 15 CCTGGACGGTGCTAC 1

RESULT 10  
US-09-873-075A-4/C  
; Sequence 4, Application US/09873075A  
; Patent No. US20020123123A1  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Schroder Glad, Sanne  
; APPLICANT: Fukuyama, Shiro  
; APPLICANT: Matsui, Tomoko  
; TITLE OF INVENTION: Cutinase variants  
; FILE REFERENCE: 10038.200-US  
; CURRENT APPLICATION NUMBER: US/09/873,075A  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-873-075A-4

Alignment Scores:  
Pred. No.: 3.49e+03 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-873-075A-4 (1-16)

QY 70 LeuAspProGlyArg 74  
|||||  
DB 16 CTGGATCCAGGGCGT 2

RESULT 11  
US-09-781-988-101  
; Sequence 101, Application US/09781988  
; Patent No. US20020150881A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsey  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20020150881A1e1  
Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W.  
Suite 300  
CITY: Washington,  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 4.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/781,988  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/664,989  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 07/487,063  
FILING DATE: 02-MAR-1990  
APPLICATION NUMBER: 07/240,160  
FILING DATE: 02-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Iver P.  
REGISTRATION NUMBER: 28005  
REFERENCE/DOCKET NUMBER: LADNER 7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-09-781-988-101

Alignment Scores:  
Pred. No.: 3.49e+03 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-781-988-101 (1-16)

QY 178 ArgileLeuPro 182  
Db 1 CGGATCCTCTCCT 15

RESULT 12

US-09-771-933-189/c  
; Sequence 189, Application US/09771933  
; Publication No. US20030023387A1  
; GENERAL INFORMATION:  
; APPLICANT: Gill-Garrison, Rosalynn D  
; APPLICANT: Martin, Christopher J  
; APPLICANT: Sanchez-Felix, Manuel V  
; TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk  
; FILE OF INVENTION: Factors  
; FILE REFERENCE: 620-130  
; CURRENT APPLICATION NUMBER: US/09/771,933  
; CURRENT FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 189  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe  
US-09-771-933-189

Alignment Scores:  
Pred. No.: 3.49e+03 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-771-933-189 (1-16)

QY 25 ArgGluThrTyLeu 29  
Db 16 AGGAGACGTATTG 2

RESULT 13

US-09-893-878-101  
; Sequence 101, Application US/09893878  
; Publication No. US20030113717A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsey  
; Markland, William  
; Lev, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20030113717A1e1  
; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/893,878  
; FILING DATE: 29-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/009,319  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 07/664,989  
; FILING DATE: 01-MAR-1991  
; APPLICATION NUMBER: PCT/US89/03731  
; FILING DATE: 01-SEP-1989  
; APPLICATION NUMBER: 07/487,063  
; FILING DATE: 02-MAR-1990  
; APPLICATION NUMBER: 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28005  
; REFERENCE/DOCKET NUMBER: LADNER 7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: genomic DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-09-893-878-101

Alignment Scores:  
Pred. No.: 3.49e+03 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-893-878-101 (1-16)

QY 178 ArgileLeuPro 182  
Db 1 CGGATCCTCTCCT 15

RESULT 14

US-09-896-095-101  
; Sequence 101, Application US/09896095  
; Publication No. US20030219886A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, Charles C.  
; APPLICANT: GUTERMAN, Sonia K.  
; APPLICANT: ROBERTS, Bruce L.  
; APPLICANT: MARKLAND, William  
; APPLICANT: LEV, Arthur C.  
; APPLICANT: KENT, Rachel B.  
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS  
; FILE REFERENCE: LADNER=7L  
; CURRENT APPLICATION NUMBER: US/09/896,095  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 08/415,922  
; PRIOR FILING DATE: 1995-03-04  
; PRIOR APPLICATION NUMBER: 08/009,319  
; PRIOR FILING DATE: 1993-01-26  
; PRIOR APPLICATION NUMBER: 07/664,989  
; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 08/993,776  
; PRIOR FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 101  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic, DNA for ID 10, lower strand, see also ID 16  
US-09-896-095-101

Alignment Scores: 3.49e-03 Length: 16  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 11

US-09-966-880A-8 (1-198) x US-09-896-095-101 (1-16)

Qy 178 ArgileLeuLeuPro 182  
Db 1 CGGATCCTCTCCCT 15

## RESULT 15

US-10-126-685-101  
; Sequence 101, Application US/10126685  
; Publication No. US20030219722A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsey  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20030219722A1e1  
; Binding Proteins

NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W.

Suite 300

CITY: Washington,

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/126,685

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/009,319

FILING DATE: 1993-01-26

APPLICATION NUMBER: 07/664,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 07/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28005

REFERENCE/DOCKET NUMBER: LADNER 7

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-126-685-101

Alignment Scores: 3.49e-03 Length: 16  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 15

US-09-966-880A-8 (1-198) x US-10-126-685-101 (1-16)

Qy 178 ArgileLeuLeuPro 182  
Db 1 CGGATCCTCTCCCT 15

## RESULT 16

US-10-127-028-101  
; Sequence 101, Application US/10127028  
; Publication No. US20040005539A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsey  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20040005539A1e1  
; Binding Proteins

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W.

Suite 300

CITY: Washington,

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,028

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/009,319

FILING DATE: 1993-01-26

APPLICATION NUMBER: 07/664,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 07/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28005

REFERENCE/DOCKET NUMBER: LADNER 7

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-127-028-101



Alignment Scores:  
Pred. No.: 3.49e+03 16  
Score: 5.00 5  
Matches: 0  
Percent Similarity: 100.00% 0  
Best Local Similarity: 100.00% 0  
Query Match: 2.53% 0  
DB: 15 0

US-09-966-880A-8 (1-198) x US-10-127-028-101 (1-16)

QY 178 ArgileLeuPro 182  
Db 1 CGGATCCTCTCCCT 15

RESULT 17

US-10-126-544-101  
; Sequence 101, Application US/10126544  
; Publication No. US20040023205A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsay  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20040023205A1e1  
; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/126,544  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/009,319  
; FILING DATE: 1993-01-26  
; APPLICATION NUMBER: 07/664,989  
; FILING DATE: 01-MAR-1991  
; APPLICATION NUMBER: PCT/US89/03731  
; FILING DATE: 01-SEP-1989  
; APPLICATION NUMBER: 07/487,063  
; FILING DATE: 02-MAR-1990  
; APPLICATION NUMBER: 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28005  
; REFERENCE/DOCKET NUMBER: LADNER 7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: circular  
; MOLECULE TYPE: genomic DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Alignment Scores:  
Pred. No.: 3.49e+03 16  
Score: 5.00 5  
Matches: 0  
Percent Similarity: 100.00% 0  
Best Local Similarity: 100.00% 0  
Query Match: 2.53% 0  
DB: 16 0

US-09-966-880A-8 (1-198) x US-10-126-544-101 (1-16)

QY 178 ArgileLeuPro 182  
Db 1 CGGATCCTCTCCCT 15

RESULT 18

US-09-866-108-9581/c  
; Sequence 9581, Application US/09866108  
; Patent No. US2002004800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 9581  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9581

Alignment Scores:  
Pred. No.: 3.69e+03 17  
Score: 5.00 5  
Percent Similarity: 100.00% 0

US-10-126-544-101

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9581 (1-17)

QY 41 SerPheSerLeuAsp 45  
DB 17 AGCTTTTCCCTCGAC 3

## RESULT 19

US-09-866-108-9582/c  
; Sequence 9582, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 9582  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9582

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9582 (1-17)

QY 41 SerPheSerLeuAsp 45  
DB 16 AGCTTTTCCCTCGAC 2

## RESULT 20

US-09-866-108-9583/c  
; Sequence 9583, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 9583  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9583

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9583 (1-17)

QY 41 SerPheSerLeuAsp 45  
DB 15 AGCTTTTCCCTCGAC 1

## RESULT 21

US-09-866-108-9630  
; Sequence 9630, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US 60/236,359  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 9630  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9630

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9630 (1-17)

Qy 124 GluglyleuArg 128  
Db 3 GAAGGGCTCGGAGG 17

## RESULT 22

US-09-866-108-9631  
; Sequence 9631, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 9631  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9631

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9631 (1-17)

Qy 124 GluglyleuArg 128  
Db 2 GAAGGGCTCGGAGG 16

## RESULT 23

US-09-866-108-9632  
; Sequence 9632, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.

```

; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9632
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-9632

Alignment Scores:
Pred. No.: 3 69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9632 (1-17)

Qy 124 GluGlyLeuArgArg 128
| | | | | | | | | | | | | | | | | | | | |
Db 1 GAAGGGCTCGGAGG 15

RESULT 24
US-09-866-108-9765
; Sequence 9765, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; CURRENT APPLICATION NUMBER: US/09/866,108

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9765
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-9765

Alignment Scores:
Pred. No.: 3 69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9765 (1-17)

Qy 103 AsnLeuSerLeuArg 107
| | | | | | | | | | | | | | | | | | | | |
Db 3 AACCTCTCGCTGAGG 17

RESULT 25
US-09-866-108-9766
; Sequence 9766, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; CURRENT APPLICATION NUMBER: US/09/866,108

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;  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 9766  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9766

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9766 (1-17)

QY 103 AsnLeuSerLeuArg 107  
|||||  
Db 2 AACCTCTCGTGAGG 16

RESULT 26

US-09-866-108-9767  
; Sequence 9767, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AECOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667

;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 9767  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9767

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9767 (1-17)

QY 103 AsnLeuSerLeuArg 107  
|||||  
Db 1 AACCTCTCGTGAGG 15

RESULT 27

US-09-825-805-345  
; Sequence 345, Application US/09825805  
; Publication No. US20030004122A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka Matulic  
; APPLICANT: Sweedler, Dave  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle  
; FILE REFERENCE: MEH800-831-F (400/009)  
; CURRENT APPLICATION NUMBER: US/09/825,805  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/578,223  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 09/476,387  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/064,866  
; PRIOR FILING DATE: 1997-11-05

; NUMBER OF SEQ ID NOS: 1558  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 345  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-825-805-345

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-825-805-345 (1-17)

Qy 89 AspCysAlaArgHis 93  
Db 3 GAUUGUGCGAGGCAC 17

RESULT 28

US-09-730-289B-634/c  
; Sequence 634, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MBH00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 634  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-730-289B-634

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-730-289B-634 (1-17)

Qy 165 LeuHisGluAsnSer 169  
Db 16 CTACATGAGAAATCT 2

RESULT 29

US-09-818-875-1415  
; Sequence 1415, Application US/09818875  
; Publication No. US20030051270A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27

; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 1415  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-1415

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-1415 (1-17)

Qy 129 LeuHisArgAlaGly 133  
Db 2 CTGCACCGGCGCGG 16

RESULT 30

US-09-818-875-1416/c  
; Sequence 1416, Application US/09818875  
; Publication No. US20030051270A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 1416  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-1416

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-1416 (1-17)

Qy 129 LeuHisArgAlaGly 133  
Db 16 CTGCACCGGCGCGG 2

RESULT 31

US-09-818-875-3818/c

; Sequence 3818, Application US/09818875  
; Publication No. US20030051270A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; TITLE OF INVENTION: Stranded Oligonucleotides  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 3818  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-3818

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-3818 (1-17)

Qy 93 HisValAlaAspPhe 97  
|||  
Db 15 CATGTCGACACTTT 1

RESULT 32

US-09-818-875-3819  
; Sequence 3819, Application US/09818875  
; Publication No. US20030051270A1  
; GENERAL INFORMATION:  
; APPLICANT: Kmiec, Eric B.  
; APPLICANT: Gamper, Howard B.  
; APPLICANT: Rice, Michael C.  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
; TITLE OF INVENTION: Stranded Oligonucleotides  
; FILE REFERENCE: Napro-4  
; CURRENT APPLICATION NUMBER: US/09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,176  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,179  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 4385  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 3819  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-818-875-3819

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-3819 (1-17)

Qy 93 HisValAlaAspPhe 97  
|||  
Db 3 CATGTCGACACTTT 17

RESULT 33

US-09-780-533A-382/c  
; Sequence 382, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeblerli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 382  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-382

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-382 (1-17)

Qy 169 SerValArgLeuSer 173  
|||  
Db 16 TCAGTGAGACTTTCT 2

RESULT 34

US-09-780-533A-1219/c  
; Sequence 1219, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeblerli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1219  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-1219

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1219 (1-17)

Qy 58 GlulLeuLeuPheLeu 62  
Db 16 GAGCTTCTGTTTCTT 2

## RESULT 35

US-09-780-533A-1263/c  
; Sequence 1263, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1263  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-1263

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1263 (1-17)

Qy 169 SerValArgLeuSer 173  
Db 15 TCAGTGAGACTTCT 1

## RESULT 36

US-09-780-533A-1373/c  
; Sequence 1373, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1373  
; LENGTH: 17  
; TYPE: RNA

; ORGANISM: Homo sapiens  
US-09-780-533A-1373

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1373 (1-17)

Qy 194 ArgThrLeuGlyLeu 198  
Db 17 AGAACTTGGGTTTA 3

## RESULT 37

US-09-780-533A-1374/c  
; Sequence 1374, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1374  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-1374

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1374 (1-17)

Qy 194 ArgThrLeuGlyLeu 198  
Db 16 AGAACTTGGGTTTA 2

## RESULT 38

US-09-780-533A-2240  
; Sequence 2240, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0



```
; SEQ ID NO 2240
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2240

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-2240 (1-17)
QY 8 ArgArgLysPheLeu 12
Db 1 AGGAGAAAUAUCCUU 15

RESULT 39
US-09-780-533A-2555/c
; Sequence 2555, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowhiza, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00-878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2555
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2555

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-2555 (1-17)
QY 58 GluLeuLeuPheLeu 62
Db 15 GAGCTTCGTCTCTT 1

RESULT 40
US-09-877-478-280
; Sequence 280, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
```

```
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-280

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-280 (1-17)
QY 172 LeuSerArgGlnLeu 176
Db 3 CUUUCUGGCACUU 17

RESULT 41
US-09-877-478-373
; Sequence 373, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
```

US-09-877-478-373

Alignment Scores:

Pred. No.:	3.69e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-877-478-373 (1-17)

Qy 194 ArgThrLeuGlyLeu 198

Db 3 AGGACUCUUGGACUU 17

RESULT 42

US-09-877-478-374  
 ; Sequence 374, Application US/09877478  
 ; Publication No. US20030068301A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Draper, Kenneth  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Morrissey, Dave  
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
 ; FILE REFERENCE: MEHB00-845-H (400/029)  
 ; CURRENT APPLICATION NUMBER: US/09/877,478  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR FILING DATE: 1992-05-14  
 ; PRIOR APPLICATION NUMBER: US 09/531,025  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/636,385  
 ; PRIOR FILING DATE: 2000-08-09  
 ; PRIOR APPLICATION NUMBER: US 09/696,347  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 08/193,627  
 ; PRIOR FILING DATE: 1994-02-07  
 ; PRIOR APPLICATION NUMBER: US 08/433,993  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 08/434,504  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 09/436,430  
 ; PRIOR FILING DATE: 1999-11-08  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 374  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Hepatitis B virus  
 ; US-09-877-478-374

Alignment Scores:

Pred. No.:	3.69e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-877-478-374 (1-17)

Qy 194 ArgThrLeuGlyLeu 198

Db 1 AGGACUCUUGGACUU 15

RESULT 43

US-09-877-478-1106  
 ; Sequence 1106, Application US/09877478  
 ; Publication No. US20030068301A1  
 ; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Draper, Kenneth  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Morrissey, Dave  
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
 ; FILE REFERENCE: MEHB00-845-H (400/029)  
 ; CURRENT APPLICATION NUMBER: US/09/877,478  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: US 07/882,712  
 ; PRIOR FILING DATE: 1992-05-14  
 ; PRIOR APPLICATION NUMBER: US 09/531,025  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/636,385  
 ; PRIOR FILING DATE: 2000-08-09  
 ; PRIOR APPLICATION NUMBER: US 09/696,347  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 08/193,627  
 ; PRIOR FILING DATE: 1994-02-07  
 ; PRIOR APPLICATION NUMBER: US 08/433,993  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 08/434,504  
 ; PRIOR FILING DATE: 1995-05-04  
 ; PRIOR APPLICATION NUMBER: US 09/436,430  
 ; PRIOR FILING DATE: 1999-11-08  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1106  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Hepatitis B virus  
 ; US-09-877-478-1106

Alignment Scores:

Pred. No.:	3.69e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-877-478-1106 (1-17)

Qy 194 ArgThrLeuGlyLeu 198

Db 2 AGGACUCUUGGACUU 16

RESULT 44

US-09-877-478-1486  
 ; Sequence 1486, Application US/09877478  
 ; Publication No. US20030068301A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Draper, Kenneth  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Morrissey, Dave  
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
 ; FILE REFERENCE: MEHB00-845-H (400/029)  
 ; CURRENT APPLICATION NUMBER: US/09/877,478  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: US 07/882,712  
 ; PRIOR FILING DATE: 1992-05-14  
 ; PRIOR APPLICATION NUMBER: US 09/531,025  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/636,385  
 ; PRIOR FILING DATE: 2000-08-09  
 ; PRIOR APPLICATION NUMBER: US 09/696,347  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 08/193,627  
 ; PRIOR FILING DATE: 1994-02-07  
 ; PRIOR APPLICATION NUMBER: US 08/433,993  
 ; PRIOR FILING DATE: 1995-05-04

; PRIOR APPLICATION NUMBER: US 08/434,504  
; PRIOR FILING DATE: 1995-05-04  
; PRIOR APPLICATION NUMBER: US 09/436,430  
; PRIOR FILING DATE: 1999-11-08  
; NUMBER OF SEQ ID NOS: 6586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1486  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Hepatitis B virus  
US-09-877-478-1486

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-1486 (1-17)

QY 172 LeuSerArgGlnLeu 176  
|||||  
Db 2 CUUUCUGGCAACU 16

## RESULT 45

US-09-848-754A-967/c  
; Sequence 967, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 967  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-967

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-967 (1-17)

QY 129 LeuHisArgAlaGly 133  
|||||  
Db 17 TTGCACAGGCGCAGG 3

## RESULT 46

US-09-848-754A-968/c  
; Sequence 968, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 968

; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-968

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-968 (1-17)

QY 129 LeuHisArgAlaGly 133  
|||||  
Db 16 TTGCACAGGCGCAGG 2

## RESULT 47

US-09-848-754A-969/c  
; Sequence 969, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 969  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-969

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-969 (1-17)

QY 129 LeuHisArgAlaGly 133  
|||||  
Db 15 TTGCACAGGCGCAGG 1

## RESULT 48

US-09-848-754A-2430/c  
; Sequence 2430, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2430  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-848-754A-2430

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-2430 (1-17)

QY 127 ArgArgLeuHisArg 131  
|||||  
DB 15 CGTAGGCTTCATCGA 1

## RESULT 49

US-09-864-636A-789  
; Sequence 789, Application US/09864636A  
; Publication No. US20030104378A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Allwail, Hatim  
; APPLICANT: Bartholomay, Christian  
; APPLICANT: Chehak, LuAnne  
; TITLE OF INVENTION: Detection of RNA Sequences  
; FILE REFERENCE: FORS-04944  
; CURRENT APPLICATION NUMBER: US/09/864,636A  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 2640  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 789  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-864-636A-789

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-636A-789 (1-17)

QY 70 LeuAspProGlyArg 74  
|||||  
DB 2 CTTGACCCAGGAGG 16

## RESULT 50

US-09-864-636A-794  
; Sequence 794, Application US/09864636A  
; Publication No. US20030104378A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Allwail, Hatim  
; APPLICANT: Bartholomay, Christian  
; APPLICANT: Chehak, LuAnne  
; TITLE OF INVENTION: Detection of RNA Sequences  
; FILE REFERENCE: FORS-04944  
; CURRENT APPLICATION NUMBER: US/09/864,636A  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 2640  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 794  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-864-636A-794

Alignment Scores:

Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-636A-794 (1-17)

QY 70 LeuAspProGlyArg 74  
|||||  
DB 2 CTTGACCCAGGAGG 16

## RESULT 51

US-09-740-332-1533  
; Sequence 1533, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; FILE REFERENCE: RPI 4007003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1533  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-1533

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-740-332-1533 (1-17)

QY 126 LeuArgArgLeuHis 130  
|||||  
DB 1 CUGAGGAGGUCCAU 15

## RESULT 52

US-09-817-879-1533  
; Sequence 1533, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; FILE REFERENCE: MHHB00-801-P  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1533  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-1533

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-817-879-1533 (1-17)

QY 126 LeuArgProGlyArg 130  
|||||  
Db 1 CUGAGGAGGCUCCAU 15

RESULT 53  
US-09-864-426A-789  
; Sequence 789, Application US/09864426A  
; Publication No. US20040018489A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Ma, Wu Po  
; APPLICANT: Lyamichiev, Victor  
; APPLICANT: Saiser, Michael  
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences  
; FILE REFERENCE: FORS-04946  
; CURRENT APPLICATION NUMBER: US/09/864,426A  
; CURRENT FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 2640  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 789  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic

US-09-864-426A-789

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-426A-789 (1-17)

QY 70 LeuArgProGlyArg 74  
|||||  
Db 2 CTTGACCCAGGAGG 16

RESULT 54  
US-09-864-426A-794  
; Sequence 794, Application US/09864426A  
; Publication No. US20040018489A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Ma, Wu Po  
; APPLICANT: Lyamichiev, Victor  
; APPLICANT: Saiser, Michael  
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences  
; FILE REFERENCE: FORS-04946  
; CURRENT APPLICATION NUMBER: US/09/864,426A  
; CURRENT FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 2640  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 794  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic

US-09-864-426A-794

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-426A-794 (1-17)

QY 70 LeuArgProGlyArg 74  
|||||  
Db 2 CTTGACCCAGGAGG 16

RESULT 55  
US-10-297-134B-40/c  
; Sequence 40, Application US/10297134B  
; Publication No. US20040038233A1  
; GENERAL INFORMATION:  
; APPLICANT: Biomedlab  
; TITLE OF INVENTION: diagnosis kit for Mycobacterium species identification and  
; FILE REFERENCE: drug-resistance detection and manufacturing method thereof  
; FILE REFERENCE: SGG1601PCT  
; CURRENT APPLICATION NUMBER: US/10/297,134B  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: KR10-2000-0029369  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 40  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Mycobacterium fortuitum, M. flavescens

US-10-297-134B-40

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-297-134B-40 (1-17)

QY 174 ArgGlnLeuArgArg 178  
|||||  
Db 17 CGACAGCTGCACGT 3

RESULT 56  
US-10-060-756A-1206  
; Sequence 1206, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1206  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-1206

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1206 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 3 CTTTCCAGACACTG 17

## RESULT 57

US-10-060-756A-1207  
; Sequence 1207, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1207  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-1208

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1208 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 3 CTTTCCAGACACTG 17

US-10-060-756A-1207  
; Sequence 1207, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1207  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-1208

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1207 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 2 CTTTCCAGACACTG 16

RESULT 58  
US-10-060-756A-1208  
; Sequence 1208, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1208  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-1208

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1208 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 1 CTTTCCAGACACTG 15

## RESULT 59

US-10-163-552-111  
; Sequence 111, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to lev  
; FILE REFERENCE: MEB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 111  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-111

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1208 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 1 CTTTCCAGACACTG 15

## RESULT 59

US-10-163-552-111  
; Sequence 111, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to lev  
; FILE REFERENCE: MEB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 111  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-111

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1208 (1-17)

Qy 172 LeuSerArgGlnLeu 176  
|||  
Db 1 CTTTCCAGACACTG 15

## RESULT 59

US-10-163-552-111  
; Sequence 111, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to lev  
; FILE REFERENCE: MEB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 111  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-111

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-163-552-111 (1-17)  
QY 89 AspCysAlaArchHis 93  
DB 3 GAUUGUGCGAGGCAC 17  
RESULT 60  
US-10-156-306-247  
; Sequence 247, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 247  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-247  
Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-156-306-247 (1-17)  
QY 3 SerLeuLeuMetAsn 7  
DB 1 UCGUGUCUUAUGAAU 15  
RESULT 61  
US-10-156-306-1470  
; Sequence 1470, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1470  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-1470  
Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-156-306-1470 (1-17)

QY 3 SerLeuLeuMetAsn 7  
DB 2 UCGUGUCUUAUGAAU 16  
RESULT 62  
US-10-156-306-5016/c  
; Sequence 5016, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5016  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-5016  
Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-156-306-5016 (1-17)  
QY 70 LeuAspProGlyArg 74  
DB 17 CTCGATCCTGCGCGA 3  
RESULT 63  
US-10-156-306-7033/c  
; Sequence 7033, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7033  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-7033  
Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-156-306-7033 (1-17)  
QY 70 LeuAspProGlyArg 74  
DB 16 CTCGATCCTGCGCGA 2  
RESULT 64

US-10-156-306-7034/c  
; Sequence 7034, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: MCSwigen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MEH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7034  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-7034

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-306-7034 (1-17)  
Qy 70 LeuAspProGlyArg 74  
Db 15 CTCGATCTGGCCGA 1

RESULT 65  
US-10-257-213-14  
; Sequence 14, Application US/10257213  
; Publication No. US20030129733A1  
; GENERAL INFORMATION:  
; APPLICANT: DENNING, David Wemys  
; APPLICANT: BROOKMAN, Jayne Louise  
; APPLICANT: RICKERS, Andre  
; APPLICANT: BIRCH, Mike  
; TITLE OF INVENTION: MUTANT BANK  
; FILE REFERENCE: 31229-183869  
; CURRENT APPLICATION NUMBER: US/10/257,213  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: GB0008748.6 PCT/GB01/01626  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Aspergillus fumigatus  
US-10-257-213-14

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-257-213-14 (1-17)  
Qy 176 LeuArgGileLeu 180  
Db 3 TTGAGCGAATTC 17

RESULT 66  
US-10-339-782-104  
; Sequence 104, Application US/10339782

Publication No. US20030166026A1  
; GENERAL INFORMATION:  
; APPLICANT: Lytx Therapeutics, Inc.  
; APPLICANT: Goodman, Laurie J  
; APPLICANT: Bowen, Benjamin A  
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells  
; FILE REFERENCE: 37-000110US  
; CURRENT APPLICATION NUMBER: US/10/339,782  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 104  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-782-104

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-339-782-104 (1-17)  
Qy 179 IleLeuLeuProLeu 183  
Db 2 ATCCTTCGCTCTG 16

RESULT 67  
US-10-061-201-1460  
; Sequence 1460, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 1460  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1460

Alignment Scores:  
Pred. No.: 3.69e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0



Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1460 (1-17)

OY 21 AlaLysGlyArg 25  
 DB 3 GCAAAAGGGAAGG 17

RESULT 68

US-10-061-201-1461  
 ; Sequence 1461, Application US/10061201  
 ; Publication No. US20030166229A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shannon, Mark  
 ; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
 ; FILE REFERENCE: PB0178  
 ; CURRENT APPLICATION NUMBER: US/10/061,201  
 ; PRIORITY FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/328,205  
 ; NUMBER OF SEQ ID NOS: 4162  
 ; SOFTWARE: Aeonica Sequence Listing Engine  
 ; SEQ ID NO 1461  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-061-201-1461

Alignment Scores:  
 Pred. No.: 3.69e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1461 (1-17)

OY 21 AlaLysGlyArg 25  
 DB 2 GCAAAAGGGAAGG 16

RESULT 69

US-10-061-201-1462  
 ; Sequence 1462, Application US/10061201  
 ; Publication No. US20030166229A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shannon, Mark  
 ; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
 ; FILE REFERENCE: PB0178  
 ; CURRENT APPLICATION NUMBER: US/10/061,201  
 ; PRIORITY FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/328,205  
 ; NUMBER OF SEQ ID NOS: 4162  
 ; SOFTWARE: Aeonica Sequence Listing Engine  
 ; SEQ ID NO 1462  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-061-201-1462

Alignment Scores:  
 Pred. No.: 3.69e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1462 (1-17)

OY 21 AlaLysGlyArg 25  
 DB 1 GCAAAAGGGAAGG 15

RESULT 70

US-10-084-839-789  
 ; Sequence 789, Application US/10084839  
 ; Publication No. US20030186238A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Third Wave Technologies  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Argue, Brad T.  
 ; APPLICANT: Bartholomay, Christian T.  
 ; APPLICANT: Chehak, LuAnne  
 ; APPLICANT: Curtis, Michelle L.  
 ; APPLICANT: Eis, Peggy S.  
 ; APPLICANT: Hall, Jeff G.  
 ; APPLICANT: IP, Ron S.  
 ; APPLICANT: Ji, Lin  
 ; APPLICANT: Kaiser, Michael  
 ; APPLICANT: Kwiatkowski, Jr., Robert W.  
 ; APPLICANT: Lukowiak, Andrew A.  
 ; APPLICANT: Lyamichev, Victor  
 ; APPLICANT: Lyamacheva, Natalie E.  
 ; APPLICANT: Ma, WuPo  
 ; APPLICANT: Neri, Bruce P.  
 ; APPLICANT: Olson, Sarah M.  
 ; APPLICANT: Olson-Munoz, Marilyn C.  
 ; APPLICANT: Schaefer, James J.  
 ; APPLICANT: Skrzypczynski, Zbigniew  
 ; APPLICANT: Takova, Tsetska Y.  
 ; APPLICANT: Thompson, Lisa C.  
 ; APPLICANT: Vedvik, Kevin L.  
 ; TITLE OF INVENTION: RNA Detection Assays  
 ; FILE REFERENCE: FORS-06666  
 ; CURRENT APPLICATION NUMBER: US/10/084,839

; CURRENT FILING DATE: 2002-02-26  
 ; NUMBER OF SEQ ID NOS: 4004  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 789  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-10-084-839-789

Alignment Scores:  
 Pred. No.: 3.69e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-839-789 (1-17)

QY 70 LeuAspProGlyArg 74  
 DB 2 CTTGACCCAGGAGG 16

## RESULT 71

US-10-084-839-794  
 ; Sequence 794, Application US/10084839  
 ; Publication No. US20030186238A1

; GENERAL INFORMATION:  
 ; APPLICANT: Third Wave Technologies  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Argue, Brad T.  
 ; APPLICANT: Bartholomay, Christian T.  
 ; APPLICANT: Chehak, LuAnne  
 ; APPLICANT: Curtis, Michelle L.  
 ; APPLICANT: Eis, Peggy S.  
 ; APPLICANT: Hall, Jeff G.  
 ; APPLICANT: IP, Hon S.  
 ; APPLICANT: Ji, Lin  
 ; APPLICANT: Kaiser, Michael  
 ; APPLICANT: Kwiatkowski, Jr., Robert W.  
 ; APPLICANT: Lukowiak, Andrew A.  
 ; APPLICANT: Lymaicheva, Victor  
 ; APPLICANT: Ma, WuPo  
 ; APPLICANT: Ma, WuPo  
 ; APPLICANT: Neri, Bruce P.  
 ; APPLICANT: Olson, Sarah M.  
 ; APPLICANT: Olson-Munoz, Marilyn C.  
 ; APPLICANT: Schaefer, James J.  
 ; APPLICANT: Skrzypczynski, Zbigniew  
 ; APPLICANT: Takova, Tsetska Y.  
 ; APPLICANT: Thompson, Lisa C.  
 ; APPLICANT: Vedvik, Kevin L.  
 ; TITLE OF INVENTION: RNA Detection Assays  
 ; FILE REFERENCE: FORS-06666  
 ; CURRENT APPLICATION NUMBER: US/10/084,839  
 ; CURRENT FILING DATE: 2002-02-26  
 ; NUMBER OF SEQ ID NOS: 4004  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 794  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic

Alignment Scores:  
 Pred. No.: 3.69e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-839-794 (1-17)

QY 70 LeuAspProGlyArg 74  
 DB 2 CTTGACCCAGGAGG 16

## RESULT 72

US-10-084-839-4004/c  
 ; Sequence 4004, Application US/10084839  
 ; Publication No. US20030186238A1

; GENERAL INFORMATION:  
 ; APPLICANT: Third Wave Technologies  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Argue, Brad T.  
 ; APPLICANT: Bartholomay, Christian T.  
 ; APPLICANT: Chehak, LuAnne  
 ; APPLICANT: Curtis, Michelle L.  
 ; APPLICANT: Eis, Peggy S.  
 ; APPLICANT: Hall, Jeff G.  
 ; APPLICANT: IP, Hon S.  
 ; APPLICANT: Ji, Lin  
 ; APPLICANT: Kaiser, Michael  
 ; APPLICANT: Kwiatkowski, Jr., Robert W.  
 ; APPLICANT: Lukowiak, Andrew A.  
 ; APPLICANT: Lymaicheva, Victor  
 ; APPLICANT: Ma, WuPo  
 ; APPLICANT: Ma, WuPo  
 ; APPLICANT: Neri, Bruce P.  
 ; APPLICANT: Olson, Sarah M.  
 ; APPLICANT: Olson-Munoz, Marilyn C.  
 ; APPLICANT: Schaefer, James J.  
 ; APPLICANT: Skrzypczynski, Zbigniew  
 ; APPLICANT: Takova, Tsetska Y.  
 ; APPLICANT: Thompson, Lisa C.  
 ; APPLICANT: Vedvik, Kevin L.  
 ; TITLE OF INVENTION: RNA Detection Assays  
 ; FILE REFERENCE: FORS-06666  
 ; CURRENT APPLICATION NUMBER: US/10/084,839  
 ; CURRENT FILING DATE: 2002-02-26  
 ; NUMBER OF SEQ ID NOS: 4004  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4004  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic

Alignment Scores:  
 Pred. No.: 3.69e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-839-4004 (1-17)

QY 178 ArgIleLeuPro 182  
 DB 17 CGAATTTACTTCT 3

## RESULT 73

US-10-209-787-1415  
 ; Sequence 1415, Application US/10209787  
 ; Publication No. US20030217377A1

; GENERAL INFORMATION:  
 ; APPLICANT: Kmiec, Eric B.  
 ; APPLICANT: Gamper, Howard B.

```

Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 2.53%                Indels: 0
DB: 15                            Gaps: 0

US-09-966-880A-8 (1-198) x US-10-209-787-1416 (1-17)

Qy 129 LeuHisArgAlaGly 133
   |||||
Db 16 CTGCACCGGGCCGGG 2

RESULT 75
US-10-209-787-3818/c
; Sequence 3818, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3818
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-3818

Alignment Scores:
Pred. No.: 3.69e+03      Length: 17
Score: 5.00             Matches: 17
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 2.53%                Indels: 0
DB: 15                            Gaps: 0

US-09-966-880A-8 (1-198) x US-10-209-787-3818 (1-17)

Qy 93 HisValAlaAspHe 97
   |||||
Db 15 CATGTTGCACACTT 1

RESULT 76
US-10-209-787-3819
; Sequence 3819, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179

```

```
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3819
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-3819

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-209-787-3819 (1-17)

QY 93 HisValAlaAspPhe 97
Db 3 CATGTCGACACTTT 17

RESULT 77
US-10-297-068-1106/c
; Sequence 1106, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1106
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1106

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-297-068-1106 (1-17)

QY 112 ArgLeuTyrPheCys 116
Db 15 CGCTTGACTACTCTGT 1

RESULT 78
US-10-307-005-1007/c
; Sequence 1007, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
```

```
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1007
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-307-005-1007

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-307-005-1007 (1-17)

QY 32 valvalysargarg 36
Db 15 GTTGCAAAAGGAGA 1

RESULT 79
US-10-307-005-1008
; Sequence 1008, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1008
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-307-005-1008

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
```

Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0
US-09-966-880A-B (1-198) x US-10-307-005-1008 (1-1-17)			

## RESULT 83

```

US-10-261-185-1416/c
; Sequence 1416, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1416
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-1416

```

```

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

```

US-09-966-880a-8 (1-198) x US-10-261-185-1416 (1-17)

```

```

Qy 129 LeuHisArgAlagly 133

```

```

Db 16 CTGCACCGGCCGGG 2

```

## RESULT 84

```

US-10-261-185-3818/c
; Sequence 3818, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3818
; LENGTH: 17

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-3818
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

```

US-09-966-880a-8 (1-198) x US-10-261-185-3818 (1-17)

```

```

Qy 93 HisValAlaasphe 97

```

```

Db 15 CATGTCGACACTTT 1

```

## RESULT 85

```

US-10-261-185-3819
; Sequence 3819, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3819
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-3819

```

```

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

```

US-09-966-880a-8 (1-198) x US-10-261-185-3819 (1-17)

```

```

Qy 93 HisValAlaasphe 97

```

```

Db 3 CATGTCGACACTTT 17

```

## RESULT 86

```

US-08-983-605-236/c
; Sequence 236, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400

```

; CURRENT APPLICATION NUMBER: US/08/983,605A  
; CURRENT FILING DATE: 1998-05-01  
; EARLIER APPLICATION NUMBER: DE 195 25 284.5  
; EARLIER FILING DATE: 1995-06-28  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 236  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-08-983-605-236  
  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 8 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-08-983-605-236 (1-18)  
  
Qy 70 LeuAspProGlyArg 74  
Db 16 CTAGATCCCGGTGCA 2  
  
RESULT 87  
US-09-733-523-8  
; Sequence 8, Application US/09733523  
; Patent No. US20010044134A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE 25IG87  
; FILE REFERENCE: 99-89  
; CURRENT APPLICATION NUMBER: US/09/733,523  
; CURRENT FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/169,597  
; PRIOR FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-733-523-8  
  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-09-733-523-8 (1-18)  
  
Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGCG 16  
  
RESULT 88  
US-09-122-383-3  
; Sequence 3, Application US/09122383A  
; Patent No. US20020042093A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN  
; FILE REFERENCE: 97-38  
; CURRENT APPLICATION NUMBER: US/09/122,383A

; CURRENT FILING DATE: 1998-07-24  
; EARLIER APPLICATION NUMBER: 60/053,613  
; EARLIER FILING DATE: 1997-07-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC976  
US-09-122-383-3  
  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-09-122-383-3 (1-18)  
  
Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGCG 16  
  
RESULT 89  
US-09-923-246-77  
; Sequence 77, Application US/09923246  
; Patent No. US20020128446A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020128446Alax, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/923,246  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-923-246-77  
  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-09-923-246-77 (1-18)  
  
Qy 32 ValVallysArgArg 36

```
Db      2 GTTGTAAACGACGG 16
RESULT 90
US-09-969-373-3238/c
; Sequence 3238, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3238
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3238
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3238 (1-18)
QY      101 AsnProAsnLeuSer 105
Db      18 AATCCAAATCTGAGT 4
RESULT 91
US-09-969-373-3240/c
; Sequence 3240, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3240
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3240
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3240 (1-18)
QY      101 AsnProAsnLeuSer 105
Db      18 AATCCAAATCTGAGT 4
RESULT 92
US-09-969-373-3489/c
; Sequence 3489, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3489
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3489
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3489 (1-18)
QY      179 IleLeuLeuProLeu 183
Db      17 ATTCTGTGCCACTG 3
RESULT 93
US-09-969-373-3969
; Sequence 3969, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3969
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3969
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0
```



Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-969-373-3969 (1-18)  
QY 93 HisValalaasphe 97  
Db 1 CATGTAGCCGACTTC 15  
RESULT 94  
US-09-969-373-4234  
; Sequence 4234, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 4234  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-4234  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-969-373-4234 (1-18)  
QY 101 AsnProAsnLeuSer 105  
Db 4 AATCCCAATTGTCT 18  
RESULT 95  
US-09-978-600-172  
; Sequence 172, Application US/09978600  
; Publication No. US20030087858A1  
; GENERAL INFORMATION:  
; APPLICANT: HERNSTADT, CORINNA  
; PARKER, WILLIAM D.  
; DAVIS, ROBERT  
; MILLER, SCOTT W.  
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
; Animal Models for Diseases Associated With Mitochondrial  
; Defects  
; NUMBER OF SEQUENCES: 206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036-5405  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/978,600  
FILING DATE: 15-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/413,740  
FILING DATE: 30-MAR-1995  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 172:  
US-09-978-600-172  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-978-600-172 (1-18)  
QY 125 GlyLeuArgArgLeu 129  
Db 2 GGCTCAGGAGGCTC 16  
RESULT 96  
US-09-746-375-44  
; Sequence 44, Application US/09746375  
; Publication No. US20030170823A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Kindsvogel, Wayne  
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTO18  
; FILE REFERENCE: 99-106  
; CURRENT APPLICATION NUMBER: US/09/746,375  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 60/172,105  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/\*\*\*\*,\*\*\*  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-746-375-44  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.53%  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-746-375-44 (1-18)  
QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16  
RESULT 97  
US-10-010-050A-3  
; Sequence 3, Application US/10010050A  
; Publication No. US20020173624A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN  
; FILE REFERENCE: 97-38C1  
; CURRENT APPLICATION NUMBER: US/10/010,050A  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: US 60/053,613  
; PRIOR FILING DATE: 1997-07-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC976  
US-10-010-050A-3  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 13 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-010-050A-3 (1-18)  
QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16  
RESULT 98  
US-10-086-135-7  
; Sequence 7, Application US/10086135  
; Publication No. US20020182677A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Chandrasekhar, Yasmin A.  
; TITLE OF INVENTION: PANCREATIC AND OVARIAN POLYPEPTIDE  
; FILE REFERENCE: 98-24  
; CURRENT APPLICATION NUMBER: US/10/086,135  
; CURRENT FILING DATE: 2002-02-26  
; PRIOR FILING DATE: 2002-02-26  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/366,448  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-03  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/095,199  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-03  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC976  
US-10-086-135-7

Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 13 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-086-135-7 (1-18)  
QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16  
RESULT 99  
US-10-038-241-22  
; Sequence 22, Application US/10038241  
; Publication No. US20030032167A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Lofton-Day, Catherine E.  
; APPLICANT: Whitmore, Theodore E.  
; TITLE OF INVENTION: SECRETED ALPHA-HELICAL PROTEIN ZLMDA24  
; FILE REFERENCE: 00-94  
; CURRENT APPLICATION NUMBER: US/10/038,241  
; CURRENT FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/242,023  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide Sequence ZC976  
US-10-038-241-22  
Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-038-241-22 (1-18)  
QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16  
RESULT 100  
US-10-197-290-10  
; Sequence 10, Application US/10197290  
; Publication No. US20030083300A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2  
; FILE REFERENCE: RTSP-0421  
; CURRENT APPLICATION NUMBER: US/10/197,290  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 09/857,299  
; PRIOR FILING DATE: 2001-20-04  
; PRIOR APPLICATION NUMBER: PCT/US99/22083  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 10  
; LENGTH: 18

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-10

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-290-10 (1-18)
QY 59 LeuLeuPheLeuArg 63
Db 4 CTTTATTCTTAGA 18

RESULT 101
US-10-197-290-42
; Sequence 42, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2.
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/857,299
; PRIOR FILING DATE: 2001-20-04
; PRIOR APPLICATION NUMBER: PCT/US99/22083
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-42

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-290-42 (1-18)
QY 38 SerAlaThrSerPhe 42
Db 4 AGTGCTACCTCTTT 18

RESULT 102
US-10-127-816-20
; Sequence 20, Application US/10127816
; Publication No. US20030104416A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian A.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Taft, David W.
; APPLICANT: Kindsvoegel, Wayne R.
; TITLE OF INVENTION: CYTOKINE PROTEIN FAMILY
; FILE REFERENCE: 01-17
; CURRENT APPLICATION NUMBER: US/10/127,816

; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,408
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/286,482
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/341,050
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/341,105
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/285,424
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer 2C976
US-10-127-816-20

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-127-816-20 (1-18)
QY 32 ValVallyysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 103
US-10-274-638-14
; Sequence 14, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer 2C976
US-10-274-638-14

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-274-638-14 (1-18)
QY 32 ValVallyysArgArg 36
Db 2 GTTGTAACGACGG 16
```

```
Db      2 GTTGTAAACGACGG 16

RESULT 104
US-10-295-723-77
; Sequence 77, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-295-723-77

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%      Indels:         0
DB:              14        Gaps:           0

US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)
Qy      32 ValVallysArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 105
US-10-282-622-24
; Sequence 24, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-282-622-24

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%      Indels:         0
DB:              14        Gaps:           0

US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)
Qy      32 ValVallysArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 106
US-10-313-739-32
; Sequence 32, Application US/10313739
; Publication No. US20030138948A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Fisk, Gregory
; APPLICANT: Inokuma, Margaret
; TITLE OF INVENTION: Islet Cells from Human Embryonic Stem Cells
; FILE REFERENCE: 132/002
; CURRENT APPLICATION NUMBER: US/10/313,739
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/338,885
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-739-32

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%      Indels:         0
DB:              14        Gaps:           0

US-09-966-880A-8 (1-198) x US-10-313-739-32 (1-18)
Qy      194 ArgThrLeuGlyLeu 198
Db      2 AGGACCTTGGGCTG 16

RESULT 107
US-10-243-072-6
; Sequence 6, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAI1
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
```

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; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-243-072-6

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-243-072-6 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAACACGCGG 16

RESULT 108
US-10-321-164-19
; Sequence 19, Application US/10321164
; Publication No. US20030165530A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/10/321,164
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/552,225A
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-10-321-164-19

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-321-164-19 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAACACGCGG 16

RESULT 109
US-10-164-230-13
; Sequence 13, Application US/10164230
; Publication No. US20030170652A1
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
```

```
; APPLICANT: Taniwa, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112US1
; CURRENT APPLICATION NUMBER: US/10/164,230
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence
US-10-164-230-13

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-164-230-13 (1-18)
QY 128 ArgLeuHisArgAla 132
Db 4 CGCCTCCACAGCT 18

RESULT 110
US-10-197-293-12
; Sequence 12, Application US/10197293
; Publication No. US20030171547A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49C1
; CURRENT APPLICATION NUMBER: US/10/197,293
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US 09/686,838
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/140,804
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/056,983
; PRIOR FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-10-197-293-12

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-293-12 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAACACGCGG 16
```

```
RESULT 111
US-10-414-186-6
; Sequence 6, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-414-186-6

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-414-186-6 (1-18)

OY 32 ValVallyeArgArg 36
DB 2 GTGTAAACGACGG 16

RESULT 112
US-10-082-649-17
; Sequence 17, Application US/10082649
; Publication No. US20030176645A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/082,649
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

RESULT 113
US-10-204-884-10
; Sequence 10, Application US/10204884
; Publication No. US20030186371A1
; GENERAL INFORMATION:
; APPLICANT: Oxagen Limited
; APPLICANT: Olaveson, Mark
; APPLICANT: Lench, Nick
; APPLICANT: Allen, Maxine
; APPLICANT: Tazi-Ahmini, Rachind
; TITLE OF INVENTION: Test and model for inflammatory disease
; FILE REFERENCE: P3000MO-PS
; CURRENT APPLICATION NUMBER: US/10/204,884
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: GB 0004312.5
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-204-884-10

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-204-884-10 (1-18)

OY 129 LeuHisArgAlaGly 133
```

```
Db      3 CTCCACAGAGCTGGA 17
|||||
RESULT 114
US-10-204-884-77
; Sequence 77, Application US/10204884
; Publication No. US20030186371A1
; GENERAL INFORMATION:
; APPLICANT: Oxagen Limited
; APPLICANT: Olaveson, Mark
; APPLICANT: Lench, Nick
; APPLICANT: Allen, Maxine
; APPLICANT: Tazi-Ahmini, Rachid
; TITLE OF INVENTION: Test and model for inflammatory disease
; FILE REFERENCE: P300000-PS
; CURRENT APPLICATION NUMBER: US/10/204,884
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: GB 0004312.5
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-204-884-77

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             15         Gaps:       0

US-09-966-880A-8 (1-198) x US-10-204-884-77 (1-18)
QY      129 LeuHisArgAlaGly 133
|||||
Db      3 CTCCACAGAGCTGGA 17
|||||
RESULT 115
US-10-388-263-163
; Sequence 163, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-163
```

```
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             15         Gaps:       0

US-09-966-880A-8 (1-198) x US-10-388-263-163 (1-18)
QY      59 LeuLeuPheLeuArg 63
|||||
Db      4 CTTTATTCTTACA 18
|||||
RESULT 116
US-10-388-263-195
; Sequence 195, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-195

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             15         Gaps:       0

US-09-966-880A-8 (1-198) x US-10-388-263-195 (1-18)
QY      38 SerAlaThrSerPhe 42
|||||
Db      4 AGTGTACCTCTTT 18
|||||
RESULT 117
US-10-388-263-244/c
; Sequence 244, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
US-10-388-263-244/c
```

```

; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-244

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-263-244 (1-18)

Qy 103 AsnLeuSerIeuArg 107
Db 17 AACCTTTCTCTCAGA 3

RESULT 118
US-10-349-143-6619
; Sequence 6619, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6619
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in compl
US-10-349-143-6619

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-6619 (1-18)

Qy 103 AsnLeuSerIeuArg 107
Db 17 AACCTTTCTCTCAGA 3

RESULT 119
US-10-349-143-10343
; Sequence 10343, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in compl
US-10-349-143-10343

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-10343 (1-18)

Qy 34 LysArgGArgSpSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 120
US-10-395-741B-44
; Sequence 44, Application US/10395741B
; Publication No. US20040023341A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: ANTI-IL-1/TIF ANTIBODIES AND METHODS OF
; FILE REFERENCE: 02-04
; CURRENT APPLICATION NUMBER: US/10/395,741B
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/366,842
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer 2C976

```



## US-10-395-741B-44

Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 16 Gaps: 0

## US-09-966-880A-8 (1-198) x US-10-395-741B-44 (1-18)

QY 32 ValVallyeArgArg 36

Db 2 GTTGTAAACGACGG 16

## RESULT 121

US-10-621-787-19  
Sequence 19, Application US/10621787  
Publication No. US20040024187A1  
GENERAL INFORMATION:  
APPLICANT: Piddington, Christopher S.  
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
FILE REFERENCE: ZACR2  
CURRENT APPLICATION NUMBER: US/10/621,787  
CURRENT FILING DATE: 2003-07-17  
PRIOR APPLICATION NUMBER: US 09/552,204  
PRIOR FILING DATE: 2000-04-19  
PRIOR APPLICATION NUMBER: US 60/130,207  
PRIOR FILING DATE: 1993-04-20  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC976  
US-10-621-787-19

Alignment Scores:  
Pred. No.: 3.9e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 16 Gaps: 0

## US-09-966-880A-8 (1-198) x US-10-621-787-19 (1-18)

QY 32 ValVallyeArgArg 36

Db 2 GTTGTAAACGACGG 16

## RESULT 122

US-09-912-014-21  
Sequence 21, Application US/09912014  
Publication No. US2003005929A1  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.; and Tu, Eugene  
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING  
MICROELECTRONIC SYSTEMS AND DEVICES FOR  
DIAGNOSTICS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA

ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/912,014  
FILING DATE: 24-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146,504  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 203/218  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 499-1500  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-912-014-21

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

## US-09-966-880A-8 (1-198) x US-09-912-014-21 (1-19)

QY 56 HisValChuleu 60

Db 2 CACGTAGAACTGCTC 16

## RESULT 123

US-10-388-703-16  
Sequence 16, Application US/10388703  
Publication No. US20040029145A1  
GENERAL INFORMATION:  
APPLICANT: Rothschild, Max  
APPLICANT: Kim, Kwan-Suk  
APPLICANT: Neuyet-Thu, Nguyen  
TITLE OF INVENTION: No. US20040029145A1 HMG A Alleles and Use of Same as Genetic M.  
FILE REFERENCE: ISURF 2900  
CURRENT APPLICATION NUMBER: US/10/388,703  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 60/364,959  
PRIOR FILING DATE: 2002-03-15  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 19  
TYPE: DNA  
ORGANISM: porcine  
US-10-388-703-16

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-703-16 (1-19)

QY 37 AspSerAlaThrSer 41  
 |||||  
 DB 2 GACTCAGCAACCTCC 16

RESULT 124

US-10-388-703-18  
 ; Sequence 19, Application US/10388703  
 ; Publication No. US20040029145A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothschild, Max  
 ; APPLICANT: Kim, Kwan-Suk  
 ; APPLICANT: Neuvelet-Thu, Nguyen  
 ; TITLE OF INVENTION: No. US20040029145A1el HMGA Alleles and Use of Same as Genetic Marker  
 ; TITLE OF INVENTION: Quality, and Feed Efficiency Traits  
 ; FILE REFERENCE: ISURF 2900  
 ; CURRENT APPLICATION NUMBER: US/10/388,703  
 ; PRIOR FILING DATE: 2003-03-14  
 ; PRIOR APPLICATION NUMBER: 60/364,959  
 ; PRIOR FILING DATE: 2002-03-15  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: porcine  
 US-10-388-703-18

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-703-18 (1-19)

QY 37 AspSerAlaThrSer 41  
 |||||  
 DB 2 GACTCAGCAACCTCC 16

RESULT 125

US-10-398-308-127/c  
 ; Sequence 127, Application US/10398308  
 ; Publication No. US20040029825A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davies, Christopher J.  
 ; APPLICANT: Schlafer, Donald H.  
 ; APPLICANT: Hill, Jonathan R.  
 ; TITLE OF INVENTION: METHODS OF MINIMIZING IMMUNOLOGICAL REJECTION OF A  
 ; TITLE OF INVENTION: NUCLEAR TRANSFER FETUS  
 ; FILE REFERENCE: 19603/3373  
 ; CURRENT APPLICATION NUMBER: US/10/398,308  
 ; CURRENT FILING DATE: 2003-04-03  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/237,673  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: PCT/US01/30925  
 ; PRIOR FILING DATE: 2001-10-03  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 127  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: BOLA Class I,  
 ; OTHER INFORMATION: Exon 3, Series B Probe  
 US-10-398-308-127

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-398-308-127 (1-19)

QY 104 LeuSerLeuArgIle 108  
 |||||  
 DB 17 CTGCTCTCCGATC 3

RESULT 126

US-10-146-575-44  
 ; Sequence 44, Application US/10146575  
 ; Publication No. US20030059800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lichter, Jay  
 ; APPLICANT: Guido, Marco  
 ; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4  
 ; FILE REFERENCE: SEQ-12P  
 ; CURRENT APPLICATION NUMBER: US/10/146,575  
 ; CURRENT FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: US/09/144,367  
 ; PRIOR FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 44  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: H. sapiens  
 US-10-146-575-44

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-146-575-44 (1-19)

QY 22 LysGlyArgGlu 26  
 |||||  
 DB 3 AAGGCGAGGAGAG 17

RESULT 127

US-10-020-695-16/c  
 ; Sequence 16, Application US/10020695  
 ; Publication No. US20030140355A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIM, Dong-Soo  
 ; APPLICANT: NAM, Yoon-Kwon  
 ; APPLICANT: NOH, Jae-Koo  
 ; TITLE OF INVENTION: EXPRESSION VECTOR CONTAINING LECTIN GENE REGULATION SITE OF MUD  
 ; TITLE OF INVENTION: LOACH  
 ; FILE REFERENCE: PPBA0566  
 ; CURRENT APPLICATION NUMBER: US/10/020,695  
 ; CURRENT FILING DATE: 2001-12-12  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Kapatentin 1.71  
 ; SEQ ID NO 16  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: primer for detecting a lectin gene regulation site of a mud loa  
 US-10-020-695-16

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-020-695-16 (1-19)

QY 162 TtGluGluLeuHis 166

Db 18 TGAGGAGGACTGCAT 4

RESULT 128

US-10-371-066-21  
; Sequence 21, Application US/10371066  
; Publication No. US20030162214A1  
; GENERAL INFORMATION:  
; APPLICANT: Heller, Michael J.; and Tu, Eugene  
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING  
; MICROELECTRONIC SYSTEMS AND DEVICES FOR  
; MOLECULAR BIOLOGICAL ANALYSIS AND  
; DIAGNOSTICS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/371,066  
; FILING DATE: 21-Feb-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,504  
; FILING DATE: NO. US20030162214A1ember 1, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 203/218  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-020-695-16 (1-19)

QY 162 TtGluGluLeuHis 166

Db 18 TGAGGAGGACTGCAT 4

RESULT 128

US-10-371-066-21  
; Sequence 21, Application US/10371066  
; Publication No. US20030162214A1  
; GENERAL INFORMATION:  
; APPLICANT: Heller, Michael J.; and Tu, Eugene  
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING  
; MICROELECTRONIC SYSTEMS AND DEVICES FOR  
; MOLECULAR BIOLOGICAL ANALYSIS AND  
; DIAGNOSTICS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/371,066  
; FILING DATE: 21-Feb-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,504  
; FILING DATE: NO. US20030162214A1ember 1, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 203/218  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-371-066-21 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-371-066-21 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16

RESULT 129

US-10-221-917-1/c  
; Sequence 1, Application US/10221917  
; Publication No. US20030171570A1

; GENERAL INFORMATION:  
; APPLICANT: Schweitzer, Markus

; TITLE OF INVENTION: Reactive Monomers For The Oligonucleotide and  
; Polynucleotide Synthesis, Modified Oligonucleotides And  
; Polynucleotides, and A Method For Producing The Same  
; FILE REFERENCE: 200404.us  
; CURRENT APPLICATION NUMBER: US/10/221,917  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: PCT/EP01/01799  
; PRIOR FILING DATE: 2001-02-19  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polynucleotides  
; OTHER INFORMATION: from modified acetals and aldehydes  
US-10-221-917-1  
Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-221-917-1 (1-19)

QY 56 HisValGluLeuLeu 60

Db 18 CACGTAGACTGCTC 4

RESULT 130

US-10-170-172-21

; Sequence 21, Application US/10170172  
; Publication No. US20030190632A1

; GENERAL INFORMATION:  
; APPLICANT: SOSNOWSKI, RONALD G

; APPLICANT: BUTLER, WILLIAM F

; APPLICANT: TU, EUGENE

; APPLICANT: NERENBERG, MICHAEL I

; APPLICANT: HELLER, MICHAEL J

; APPLICANT: EDMAN, CARL P

; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC  
; DEVICES, COMPONENT SYSTEMS, METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL  
; ANALYSIS AND DIAGNOSTICS  
; FILE REFERENCE: DAVID B. MURPHY; Nanogen 227/194  
; CURRENT APPLICATION NUMBER: US/10/170,172  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US/08/986,065  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Human

US-10-170-172-21

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

```
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-21 (1-19)

QY 56 HisValGlutLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 131
US-10-170-172-45/c
; Sequence 45, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; PRIOR FILING DATE: 2002-06-11
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human
US-10-170-172-45

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-45 (1-19)

QY 56 HisValGlutLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 132
US-10-170-172-50/c
; Sequence 50, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 50
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human
US-10-170-172-50

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-50 (1-19)

QY 56 HisValGlutLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 133
US-10-170-221-20
; Sequence 20, Application US/10170221
; Publication No. US20030192068A1
; GENERAL INFORMATION:
; APPLICANT: DeBoer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,221
; FILING DATE: 11-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,798
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 US-10-170-221-20

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-221-20 (1-19)

QY 32 ValVallyArgArg 36  
 DB 5 GTTGTAAACGACGG 19

RESULT 134

US-10-244-647-467  
 ; Sequence 467, Application US/10244647  
 ; Publication No. US20030206887A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceutical, Inc.  
 ; APPLICANT: Morrissey, David  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Beigelman, Leonid  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)  
 ; FILE REFERENCE: 400/060 (MBHB02-1000)  
 ; CURRENT FILING DATE: 2003-04-14  
 ; PRIOR APPLICATION NUMBER: US 60/358,580  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/393,924  
 ; PRIOR FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: PCT US02/09187  
 ; PRIOR FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/296,876  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 1524  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 467  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
 US-10-244-647-467

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-467 (1-19)

QY 172 LeuSerArgGlnLeu 176  
 DB 2 CUUUCUGCCACACU 16

RESULT 135

US-10-244-647-469  
 ; Sequence 469, Application US/10244647  
 ; Publication No. US20030206887A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceutical, Inc.  
 ; APPLICANT: Morrissey, David

APPLICANT: McSwiggen, James  
 APPLICANT: Beigelman, Leonid  
 TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)  
 FILE REFERENCE: 400/060 (MBHB02-1000)  
 CURRENT APPLICATION NUMBER: US/10/244,647  
 CURRENT FILING DATE: 2003-04-14  
 PRIOR APPLICATION NUMBER: US 60/358,580  
 PRIOR FILING DATE: 2002-02-20  
 PRIOR APPLICATION NUMBER: US 60/393,924  
 PRIOR FILING DATE: 2002-07-03  
 PRIOR APPLICATION NUMBER: PCT US02/09187  
 PRIOR FILING DATE: 2002-03-26  
 PRIOR APPLICATION NUMBER: US 60/296,876  
 PRIOR FILING DATE: 2001-06-08  
 NUMBER OF SEQ ID NOS: 1524  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 469  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
 US-10-244-647-469

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-469 (1-19)

QY 172 LeuSerArgGlnLeu 176  
 DB 1 CUUUCUGCCACACU 15

RESULT 136

US-10-244-647-1113/C  
 ; Sequence 1113, Application US/10244647  
 ; Publication No. US20030206887A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceutical, Inc.  
 ; APPLICANT: Morrissey, David  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Beigelman, Leonid  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)  
 ; FILE REFERENCE: 400/060 (MBHB02-1000)  
 ; CURRENT APPLICATION NUMBER: US/10/244,647  
 ; CURRENT FILING DATE: 2003-04-14  
 ; PRIOR APPLICATION NUMBER: US 60/358,580  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: US 60/393,924  
 ; PRIOR FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: PCT US02/09187  
 ; PRIOR FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/296,876  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 1524  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1113  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
 US-10-244-647-1113

Alignment Scores:  
 Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-1113 (1-19)

QY 172 LeuSerArgGlnLeu 176  
Db 18 CTTTCGCGCAACTT 4

## RESULT 137

US-10-244-647-1115/c  
; Sequence 1115, Application US/10244647  
; Publication No. US20030206887A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceutical, Inc.  
; APPLICANT: Morrissey, David  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)  
; TITLE OF INVENTION: Short Interfering Nucleic Acid (siRNA)  
; FILE REFERENCE: 400/060 (MBH02-1000)  
; CURRENT APPLICATION NUMBER: US/10/244,647  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/393,924  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: PCT US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 1524  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1115  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region  
US-10-244-647-1115

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-1115 (1-19)

QY 172 LeuSerArgGlnLeu 176  
Db 19 CTTTCGCGCAACTT 5

## RESULT 138

US-10-444-925-459  
; Sequence 459, Application US/10444925  
; Publication No. US20040009946A1  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, Stephen Patrick  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Wilson, Linda K.  
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION  
; TITLE OF INVENTION: BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.441  
; CURRENT APPLICATION NUMBER: US/10/444,925  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 459  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-925-459

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-925-459 (1-19)

QY 119 ArgLysAlaGluPro 123  
Db 4 AGGAAGCGCAGAGCCC 18

## RESULT 139

US-10-444-925-570  
; Sequence 570, Application US/10444925  
; Publication No. US20040009946A1  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, Stephen Patrick  
; APPLICANT: Klinghoffer, Richard  
; APPLICANT: Wilson, Linda K.  
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION  
; TITLE OF INVENTION: BY RNA INTERFERENCE  
; FILE REFERENCE: 200125.441  
; CURRENT APPLICATION NUMBER: US/10/444,925  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 570  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Small interfering RNA  
US-10-444-925-570

Alignment Scores:  
Pred. No.: 4.1e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-925-570 (1-19)

QY 125 GlyLeuArgGlnLeu 129  
Db 4 GGUCUGCGCGUCUA 18

## RESULT 140

US-09-764-050A-2  
; Sequence 2, Application US/09764050A  
; Patent No. US20020068282A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Detection/Quantification of Targeted Nucleotide Chains and  
; TITLE OF INVENTION: Detection/Quantification of Multi-Stranded Nucleotide Chains  
; TITLE OF INVENTION: by Fluorescence  
; FILE REFERENCE: 3495015  
; CURRENT APPLICATION NUMBER: US/09/764,050A  
; CURRENT FILING DATE: 2001-01-19  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-09-764-050A-2

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-764-050A-2 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 141
US-09-416-384A-12
; Sequence 12, Application US/09416384A
; Patent No. US20020081584A1
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BOUGUELERET, Lydie
; APPLICANT: CHUMAKOV, Ilya
; APPLICANT: COHEN, Daniel
; APPLICANT: ESSIUX, Laurent
; TITLE OF INVENTION: Genes, proteins and biallelic markers related to central....
; FILE REFERENCE: GENSET.045AUS
; CURRENT FILING DATE: 1999-10-12
; CURRENT APPLICATION NUMBER: US/09/416,384A
; PRIOR FILING DATE: 1999-10-30
; PRIOR APPLICATION NUMBER: 60/106,457
; PRIOR FILING DATE: 1999-10-30
; PRIOR APPLICATION NUMBER: 60/103,955
; PRIOR FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: 60/132,277
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent.pm
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide g713RACE5R1
US-09-416-384A-12

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-416-384A-12 (1-20)

Qy 23 GlyArgArgGluThr 27
Db 2 GGTAGAAGGGAGACT 16

RESULT 142
US-09-731-457B-79/c
; Sequence 79, Application US/09731457B
; Patent No. US20020103146A1
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt
```

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1,
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0182
; CURRENT APPLICATION NUMBER: US/09/731,457B
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-731-457B-79

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-731-457B-79 (1-20)

Qy 42 PheSerLeuAspPhe 46
Db 20 TTCTCCCTGGATTTT 6

RESULT 143
US-09-971-309-67
; Sequence 67, Application US/09971309
; Patent No. US20020106675A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-0494P
; CURRENT APPLICATION NUMBER: US/09/971,309
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-971-309-67

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-971-309-67 (1-20)

Qy 156 GluArgThrPheLys 160
```

Db 3 GAGAGAACTTCAAG 17  
RESULT 144  
US-09-781-988-104/c  
; Sequence 104: Application US/09781988  
; Patent No. US20020150881A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsay  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Barbault  
; TITLE OF INVENTION: Directed Evolution of No. US20020150881A1e1  
; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 4.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/781,988  
; FILING DATE: 14-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/664,989  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 07/487,063  
; FILING DATE: 02-MAR-1990  
; APPLICATION NUMBER: 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28005  
; REFERENCE/DOCKET NUMBER: LADNER 7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: genomic DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
US-09-781-988-104  
Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-781-988-104 (1-20)  
Qy 178 ArgilleLeuPro 182  
Db 18 CGGATCCTCTCGCT 4  
RESULT 145

US-09-900-063-6  
; Sequence 6, Application US/09900063  
; Patent No. US20020160372A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Max F.  
; Applicant: Vincent, Amy L.  
; APPLICANT: Tuggle, Christopher K.  
; TITLE OF INVENTION: Prolactin Receptor Gene as a Genetic Marker for  
; TITLE OF INVENTION: Increased Litter Size in Pigs  
; FILE REFERENCE: Prolactin receptor genetic marker  
; CURRENT APPLICATION NUMBER: US/09/900,063  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/274,655  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/812,208  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/742,805  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-01  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/022180  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-07-19  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: porcine  
US-09-900-063-6  
Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-900-063-6 (1-20)  
Qy 177 ArgArgilleLeuLeu 181  
Db 5 CGCAGATCCTCTGCTG 19  
RESULT 146  
US-09-963-875-27/c  
; Sequence 27, Application US/09963875  
; Patent No. US20020164307A1  
; GENERAL INFORMATION:  
; APPLICANT: Massachusetts General Hospital  
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treatin  
; FILE REFERENCE: Mellitus  
; FILE REFERENCE: 17633/1235  
; CURRENT APPLICATION NUMBER: US/09/963,875  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US60/169082  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/215109  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: US 60/238880  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/731261  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-963-875-27  
Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20



Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-963-875-27 (1-20)

Qy 59 LeuLeupheLeuArg 63  
Db 18 TTGCTGTTCTTCGG 4

RESULT 147  
US-09-309-196-44/c  
; Sequence 44, Application US/09309196  
; Publication No. US2003008380A1  
; GENERAL INFORMATION:  
; APPLICANT: FOWLES, Dana M.  
; APPLICANT: BROACH, Jim  
; APPLICANT: MANFREDI, John  
; APPLICANT: KLEIN, Christine  
; APPLICANT: MURPHY, Andrew J.  
; APPLICANT: PAUL, Jeremy  
; APPLICANT: TRUEHART, Joshua  
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
; NUMBER OF SEQUENCES: 119  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/309,196  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/322,137  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,328  
; FILING DATE: 31-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/041,431  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOLWKS=2C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-309-196-44

Alignment Scores: 4.3e+03 Length: 20  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 10

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-309-196-44 (1-20)

Qy 104 LeuSerLeuArgile 108  
Db 18 CTGAGTCTTCGCATC 4

RESULT 148  
US-09-931-375A-52  
; Sequence 52, Application US/09931375A  
; Publication No. US20030027151A1  
; GENERAL INFORMATION:  
; APPLICANT: WARMAN, Matthew L.  
; APPLICANT: GONG, Yaogin  
; APPLICANT: OLSEN, Bjorn R.  
; APPLICANT: RAWADI, Georges  
; APPLICANT: ROMAN-ROMAN, Sergio  
; TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY  
; TITLE OF INVENTION: OSTEOPOROSIS  
; FILE REFERENCE: 38464-0004  
; CURRENT APPLICATION NUMBER: US/09/931,375A  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/304,851  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/234,337  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/226,119  
; PRIOR FILING DATE: 2000-08-18  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 52  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-931-375A-52

Alignment Scores: 4.3e+03 Length: 20  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 10

US-09-966-880A-8 (1-198) x US-09-931-375A-52 (1-20)

Qy 168 AsnSerValArgLeu 172  
Db 4 AACAGTGTCCGGCTG 18

RESULT 149  
US-09-972-115A-26  
; Sequence 26, Application US/09972115A  
; Publication No. US20030032769A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gregg, Morin B.  
; APPLICANT: Walter, Funk D.  
; APPLICANT: Mieczyslaw, Piatyszek A.  
; TITLE OF INVENTION: A Second Mammalian Telomerase  
; FILE REFERENCE: 080/003C  
; CURRENT APPLICATION NUMBER: US/09/972,115A  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US 60/128,577  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/129,123  
; PRIOR FILING DATE: 1999-04-13  
; NUMBER OF SEQ ID NOS: 64

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/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 26
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-09-972-115A-26

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-972-115A-26 (1-20)

QY 25 ArgGluThrLeu 29
| | | | | | | | | |
DB 5 CGAGAGACTTATCTC 19

RESULT 150
US-09-953-354-47/c
; Sequence 47, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; TITLE OF INVENTION: Methods and Compositions for
; Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,354
; FILING DATE: 13-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/689,172
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-953-354-47

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
```

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-953-354-47 (1-20)

QY 104 LeuSerLeuArgIle 108
| | | | | | | | | |
DB 18 CTGAGTCTTCGCATC 4

RESULT 151
US-09-953-354-49/c
; Sequence 49, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; TITLE OF INVENTION: Methods and Compositions for
; Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,354
; FILING DATE: 13-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/689,172
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-953-354-49

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-953-354-49 (1-20)

QY 104 LeuSerLeuArgIle 108
| | | | | | | | | |
DB 18 CTGAGTCTTCGCATC 4

RESULT 152
US-09-912-014-7/c
; Sequence 7, Application US/09912014
```

```
; Publication No. US20030059929A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/912,014
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-912-014-7
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-912-014-7 (1-20)
Qy 56 HisValGluLeu 60
Db 18 CACGTAGAACTGCTC 4
RESULT 153
US-09-965-993-61
; Sequence 61, Application US/09865993
; Publication No. US20030060437A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5 EXPRESSION
; FILE REFERENCE: RTS-0175
; CURRENT APPLICATION NUMBER: US/09/865,993
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-993-61
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-865-993-61 (1-20)
Qy 39 AlaThrSerPheSer 43
Db 4 GCAACTTCTTTCTCC 18
RESULT 154
US-09-909-595-70/c
; Sequence 70, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-70
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-909-595-70 (1-20)
Qy 2 AspSerLeuMet 6
Db 15 GACAGTCTTCTCATG 1
RESULT 155
US-09-915-485-58
; Sequence 58, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/915,485
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

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US-09-915-485-58
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-915-485-58 (1-20)
Qy 42 PheSerLeuAspPhe 46
Db 3 TTCTCGTTGGACTTC 17

RESULT 156
US-09-918-187-28/c
; Sequence 28, Application US/09918187
; Publication No. US20030983282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-28
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-918-187-28 (1-20)
Qy 125 GlyLeuArgGlnLeu 129
Db 19 GGCTTGAGAGGTTA 5

RESULT 157
US-09-918-187-29/c
; Sequence 29, Application US/09918187
; Publication No. US20030983282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-29
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5

US-09-915-485-58
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-918-187-29 (1-20)
Qy 172 LeuSerArgGlnLeu 176
Db 16 CTGTCCAGGCAGCTC 2

RESULT 158
US-09-915-814-178/c
; Sequence 178, Application US/09915814
; Publication No. US20030096771A1
; GENERAL INFORMATION:
; APPLICANT: Mageline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0587
; CURRENT APPLICATION NUMBER: US/09/915,814
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-814-178
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-915-814-178 (1-20)
Qy 129 LeuHisArgAlaGly 133
Db 16 CTCATCGGCTGTGT 2

RESULT 159
US-09-933-878-104/c
; Sequence 104, Application US/09893878
; Publication No. US20030113717A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20030113717A1e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION NUMBER: US/09/893,878  
FILING DATE: 29-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,319  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 07/664,989  
FILING DATE: 01-MAR-1991  
APPLICATION NUMBER: PCT/US89/03731  
FILING DATE: 01-SEP-1989  
APPLICATION NUMBER: 07/487,063  
FILING DATE: 02-MAR-1990  
APPLICATION NUMBER: 07/240,160  
FILING DATE: 02-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Iver P.  
REGISTRATION NUMBER: 28005  
REFERENCE/DOCKET NUMBER: LADNER 7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
US-09-893-878-104

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-893-878-104 (1-20)

QY 178 ArgileLeuPro 182  
Db 18 CGGATCCTCTCCT 4

RESULT 160  
US-09-851-871-69  
Sequence 69, Application US/09851871  
Publication No. US20030176374A1  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Karras, James G.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
FILE REFERENCE: ISPH-0543  
CURRENT APPLICATION NUMBER: US/09/851,871  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: PCT/US00/14471  
PRIOR FILING DATE: 2000-05-25  
PRIOR FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 09/326,186  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 69  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Synthetic  
US-09-851-871-69  
Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-851-871-69 (1-20)  
QY 176 LeuArgileLeu 180  
Db 1 CTGCGCGAATCCTG 15

#### RESULT 161

US-09-851-871-166  
Sequence 166, Application US/09851871  
Publication No. US20030176374A1  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
FILE REFERENCE: ISPH-0543  
CURRENT APPLICATION NUMBER: US/09/851,871  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: PCT/US00/14471  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 09/326,186  
PRIOR FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 166  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-851-871-166

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-851-871-166 (1-20)

QY 176 LeuArgileLeu 180  
Db 2 CTGCGCGAATCCTG 16

#### RESULT 162

US-09-865-879-35/c  
Sequence 35, Application US/09865879  
Publication No. US20030180707A1  
GENERAL INFORMATION:  
APPLICANT: Roninson, Igor  
APPLICANT: Dokmanovic, Milos  
TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION  
FILE REFERENCE: 99,216-H  
CURRENT APPLICATION NUMBER: US/09/865,879  
CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/207,535  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Antisense primer for HIF-2alpha/ EPAS-1  
US-09-865-879-35

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-865-879-35 (1-20)

QY 43 SerLeuAaspPheCly 47  
|||  
DB 15 TCTCTGGATTCTGGG 1

## RESULT 163

US-09-896-095-104/c  
; Sequence 104, Application US/09896095  
; Publication No. US20030219886A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, Charles C.  
; APPLICANT: GUTERMAN, Sonia K.  
; APPLICANT: ROBERTS, Bruce L.  
; APPLICANT: MARKLAND, William  
; APPLICANT: LEY, Arthur C.  
; APPLICANT: KENT, Rachel B.  
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS  
; FILE REFERENCE: LADNER-7L  
; CURRENT APPLICATION NUMBER: US/09/896,095  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 08/415,922  
; PRIOR FILING DATE: 1995-03-04  
; PRIOR APPLICATION NUMBER: 08/009,319  
; PRIOR FILING DATE: 1993-01-26  
; PRIOR APPLICATION NUMBER: 07/664,989  
; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 08/993,776  
; PRIOR FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 104  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic, DNA for ID 10, M13.3X7  
US-09-896-095-104

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-896-095-104 (1-20)

QY 178 ArgileLeuPro 182  
|||  
DB 18 CGGATCTCTCTCCT 4

## RESULT 164

US-10-188-186-294/c  
; Sequence 294, Application US/10188186  
; Publication No. US20040029789A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-397C  
; CURRENT APPLICATION NUMBER: US/10/188,186  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/303046  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/360814  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/303828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/323380  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/361133  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: 60/304016  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/304502  
; PRIOR FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 60/305262  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/373881  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/305673  
; PRIOR FILING DATE: 2001-07-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: Custom  
; SEQ ID NO 294  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer  
US-10-188-186-294

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-186-294 (1-20)

Cy 94 ValAlaaspPheLeu 98  
|||  
DB 18 GTTGCTGACTTCCTG 4

## RESULT 165

US-10-005-964-4/c  
; Sequence 4, Application US/10005964  
; Publication No. US20020107219A1  
; GENERAL INFORMATION:  
; APPLICANT: Curriel, David T.  
; APPLICANT: Yamamoto, Masato  
; TITLE OF INVENTION: Adenoviral Vector Containing Cyclooxygenase-2  
; TITLE OF INVENTION: Promoter And Uses Thereof  
; FILE REFERENCE: D6384  
; CURRENT APPLICATION NUMBER: US/10/005,964  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/251,375  
; PRIOR FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 4  
; SEQ ID NO 4  
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: GAPDH antisense primer
US-10-005-964-4

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-005-964-4 (1-20)
QY 82 ThrSerTtpSerPro 86
DB 20 ACGTCGTGGAGTCGA 6

RESULT 166
US-10-136-891-25/c
; Sequence 25, Application US/10136891
; Publication No. US20030031657A1
; GENERAL INFORMATION:
; APPLICANT: Habener, Joel
; TITLE OF INVENTION: STEM CELLS AND THEIR USE IN TRANSPLANTATION
; FILE REFERENCE: 3284/1225
; CURRENT APPLICATION NUMBER: US/10/136,891
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/169,082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/215,109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/239,880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731,255
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-136-891-25

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-136-891-25 (1-20)
QY 59 LeuLeuPheLeuArg 63
DB 18 TTGCTGTTTCTTCGG 4

RESULT 167
US-10-057-550-93
; Sequence 93, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-93

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-057-550-93 (1-20)
QY 169 SerValArgLeuSer 173
DB 4 TCTGTAAAGGCTTCA 18

RESULT 168
US-10-084-406-11/c
; Sequence 11, Application US/10084406
; Publication No. US20030054525A1
; GENERAL INFORMATION:
; APPLICANT: Schwientek, Tilo
; TITLE OF INVENTION: UPD-N-Acetylglucosamine:
Galactose-beta1,3-N-Acetylgalactosamine-alpha-R / (GlcNAc
6-Phosphate-beta1,3-N-Acetylglucosamine-6-phosphate)
; TITLE OF INVENTION: Galactose-beta1,3-N-Acetylglucosamine-6-phosphate
; FILE REFERENCE: 4503/1G031
; CURRENT APPLICATION NUMBER: US/10/084,406
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/645,192
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-084-406-11

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-406-11 (1-20)
QY 125 GlyLeuArgArgLeu 129
```

```
Db      18 GGGTTGAGGACTG 4
|||||
RESULT 169
US-10-120-687-27/c
; Sequence 27, Application US/10120687
; Publication No. US20030082155A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treating
; TITLE OF INVENTION: Mellitus
; FILE REFERENCE: 3284/1235B
; CURRENT APPLICATION NUMBER: US/10/120,687
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US60/169082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/963,875
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/215109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/238880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731261
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Synthesized primer
US-10-120-687-27

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%      Indels:       0
DB:             14         Gaps:         0

US-09-966-880A-8 (1-198) x US-10-120-687-27 (1-20)

QY      59 LeuLeuPheLeuArg 63
|||||
Db      18 TTGCTGTTCTTCGG 4
|||||

RESULT 170
US-10-139-496-35
; Sequence 35, Application US/10139496
; Publication No. US20030082646A1
; GENERAL INFORMATION:
; APPLICANT: Carey, Thomas E.
; APPLICANT: Nair, Shanku S.
; APPLICANT: Gray, Jennifer P.
; TITLE OF INVENTION: Antigenic Targets of Autoimmune Sensorineural Hearing Loss (AISNH
; TITLE OF INVENTION: Development of Tests for Diagnosis and Management of AISNHL
; FILE REFERENCE: UM-6982
; CURRENT APPLICATION NUMBER: US/10/139,496
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/222,179
; PRIOR FILING DATE: 1998-12-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthesized primer

US-10-139-496-35

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%      Indels:       0
DB:             14         Gaps:         0

US-09-966-880A-8 (1-198) x US-10-139-496-35 (1-20)

QY      59 LeuLeuPheLeuArg 63
|||||
Db      18 TTGCTGTTCTTCGG 4
|||||

RESULT 171
US-10-181-107-147/c
; Sequence 147, Application US/10181107
; Publication No. US20030083295A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTSP-0325
; CURRENT APPLICATION NUMBER: US/10/181,107
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: PCT/US01/00888
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/484,617
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-107-147

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%      Indels:       0
DB:             14         Gaps:         0

US-09-966-880A-8 (1-198) x US-10-181-107-147 (1-20)

QY      41 SerPheSerLeuasp 45
|||||
Db      15 TCCTTCTCCCTGGAC 1
|||||

RESULT 172
US-10-002-491-62
; Sequence 62, Application US/10002491
; Publication No. US20030109467A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
; FILE REFERENCE: RTS-0239
; CURRENT APPLICATION NUMBER: US/10/002,491
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```



```

; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-71

Alignment Scores:
Pred. No.:          4.3e+03      Length:        20
Score:              5.00         Matches:        5
Percent Similarity: 100.00%     Conservative:   0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:        2.53%       Indels:        0
DB:                 14          Gaps:          0

US-09-966-880A-8 (1-198) x US-10-173-225B-71 (1-20)

QY      169 SerValArgLeuSer 173
Db      4 TCTGTAAAGCGTTTCA 18

RESULT 175
US-10-265-689-19
; Sequence 19, Application US/10245689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOUTILAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-265-689-19

Alignment Scores:
Pred. No.:          4.3e+03      Length:        20
Score:              5.00         Matches:        5
Percent Similarity: 100.00%     Conservative:   0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:        2.53%       Indels:        0
DB:                 14          Gaps:          0

US-09-966-880A-8 (1-198) x US-10-265-689-19 (1-20)

```

QY 22 LysGlyArgGlu 26  
 |||||  
 DB 5 AAGGGAAGGCGAA 19

## RESULT 176

US-10-265-689-30  
 ; Sequence 30, Application US/10265689  
 ; Publication No. US20030119775A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SURMIT, RICHARD S.  
 ; APPLICANT: COLLINS, SHEILA A.  
 ; APPLICANT: WARDEN, CRAIG H.  
 ; APPLICANT: SELDIN, MICHAEL F.  
 ; APPLICANT: RICQUIER, DANIEL  
 ; APPLICANT: BOULLAUD, FREDERIC  
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN  
 ; FILE REFERENCE: 1579-376  
 ; CURRENT APPLICATION NUMBER: US/10/265,689  
 ; CURRENT FILING DATE: 2002-10-08  
 ; PRIOR APPLICATION NUMBER: US/09/353,645  
 ; PRIOR FILING DATE: 1999-07-15  
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864  
 ; PRIOR FILING DATE: 1997-04-22  
 ; PRIOR APPLICATION NUMBER: 60/034,960  
 ; PRIOR FILING DATE: 1997-01-15  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 30  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US-10-265-689-30

Alignment Scores:  
 Pred. No.: 20  
 Score: 5.00  
 Length: 20  
 Matches: 5  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Query Match: 2.53%  
 Indels: 0  
 DB: 14  
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-265-689-30 (1-20)

QY 22 LysGlyArgGlu 26  
 |||||  
 DB 5 AAGGGAAGGCGAA 19

## RESULT 177

US-10-000-213-58  
 ; Sequence 58, Application US/10000213  
 ; Publication No. US20030125271A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brenda F. Baker  
 ; APPLICANT: Mark P. Roach  
 ; APPLICANT: Kenneth Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF VITAMIN D NUCLEAR RECEPTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0327  
 ; CURRENT APPLICATION NUMBER: US/10/000,213  
 ; CURRENT FILING DATE: 2001-11-14  
 ; NUMBER OF SEQ ID NOS: 94  
 ; SEQ ID NO 58  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-000-213-58

Alignment Scores:  
 Pred. No.: 4.3e+03  
 Length: 20

Score: 5.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 14  
 Matches: 5  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-000-213-58 (1-20)

QY 70 LeuAspProGlyArg 74  
 |||||  
 DB 5 TTAGACCAGGCGA 19

## RESULT 178

US-10-339-604-31  
 ; Sequence 31, Application US/10339604  
 ; Publication No. US20030152982A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DE BEENHOUWER, HANS  
 ; APPLICANT: FORTAELS, FRANCOISE  
 ; APPLICANT: NACHTELINCKX, LIEVE  
 ; APPLICANT: JANNES, GEERT  
 ; APPLICANT: ROSSAU, RUDI  
 ; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium  
 ; FILE REFERENCE: 1657.0010001  
 ; CURRENT APPLICATION NUMBER: US/10/339,604  
 ; CURRENT FILING DATE: 2003-01-10  
 ; PRIOR APPLICATION NUMBER: US/09/722,319  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: US 08/750,088  
 ; PRIOR FILING DATE: 1996-12-06  
 ; PRIOR APPLICATION NUMBER: PCT/EP95/02230  
 ; PRIOR FILING DATE: 1995-06-09  
 ; PRIOR APPLICATION NUMBER: EP 94870093.5  
 ; PRIOR FILING DATE: 1994-06-09  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 31  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-10-339-604-31

Alignment Scores:  
 Pred. No.: 4.3e+03  
 Length: 20  
 Score: 5.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: 14  
 Matches: 5  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-339-604-31 (1-20)

QY 92 ArgHisValalaasp 96  
 |||||  
 DB 4 CGGCAATGCGGAT 18

## RESULT 179

US-10-037-986-59  
 ; Sequence 59, Application US/10037986  
 ; Publication No. US20030157487A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larry Gold  
 ; APPLICANT: Craig Tuerk  
 ; TITLE OF INVENTION: Nucleic Acid Ligands  
 ; NUMBER OF SEQUENCES: 374  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado

```

/ COUNTRY: USA
/ ZIP: 80111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 8.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/037,986
/ FILING DATE: 18-Oct-2001
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/143,190
/ FILING DATE: August 27, 1998
/ APPLICATION NUMBER: 08/469,609
/ FILING DATE: June 6, 1995
/ APPLICATION NUMBER: 08/428,964
/ FILING DATE: April 25, 1995
/ APPLICATION NUMBER: 08/412,110
/ FILING DATE: March 27, 1995
/ APPLICATION NUMBER: 08/409,442
/ FILING DATE: March 24, 1995
/ APPLICATION NUMBER: 07/714,131
/ FILING DATE: June 10, 1991
/ APPLICATION NUMBER: 07/536,428
/ FILING DATE: June 11, 1990
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barry J. Swanson
/ REGISTRATION NUMBER: 33,215
/ REFERENCE/DOCKET NUMBER: NEX01/CT
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-037-986-59

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-037-986-59 (1-20)

QY 32 ValValVeaRGaRG 36
Db 4 GTGTAAACGACGG 18

RESULT 180
US-10-037-066-7/c
/ Sequence 7, Application US/10371066
/ Publication No. US20030162214A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Heller, Michael J.; and Tu, Eugene
/ TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
/ MICROELECTRONIC SYSTEMS AND DEVICES FOR
/ DIAGNOSTICS
/
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 611 West Sixth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90017

```

```

/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/371,066
/ FILING DATE: 21-Feb-2003
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/146,504
/ FILING DATE: No US20030162214A1ember 1, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 203/218
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEEX: 67-3510
/
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-371-066-7

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-371-066-7 (1-20)

QY 56 HisValGlaLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 181
US-10-133-779-78/c
/ Sequence 78, Application US/10133779
/ Publication No. US20030165894A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Chow, Robert
/ APPLICANT: Tonai, Richard
/ APPLICANT: StemCyt, Inc
/ TITLE OF INVENTION: High Throughput Methods of HLA Typing
/ FILE REFERENCE: 020035-000210US
/ CURRENT APPLICATION NUMBER: US/10/133,779
/ CURRENT FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: US/09/747,391
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/172,768
/ PRIOR FILING DATE: 1999-12-20
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Fast-SEQ for Windows Version 3.0
/
/ SEQ ID NO 78
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
/ US-10-133-779-78

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0

```

```
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-133-779-78 (1-20)
QY 112 ArgLeuTyPheCys 116
Db 20 GCCTGTACTTCTGT 6
RESULT 182
US-10-218-969-92
; Sequence 92, Application US/10218969
; Publication No. US20030165916A1
; GENERAL INFORMATION:
; APPLICANT: Sealfon, Stuart
; APPLICANT: Yuen, Tony
; APPLICANT: Wurmbach, Elisa
; TITLE OF INVENTION: Use of Intrinsic Reporters of Cell Signaling For High Content Drug
; TITLE OF INVENTION: Profiling and Toxicity Screening
; FILE REFERENCE: 2459-1-007N
; CURRENT APPLICATION NUMBER: US/10/218,969
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/312,220
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/324,895
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-969-92
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-218-969-92 (1-20)
QY 94 ValAlaAspPheLeu 98
Db 6 GTTGTGACTTCTGT 20
RESULT 183
US-10-388-307-11/c
; Sequence 11, Application US/10388307
; Publication No. US20030180778A1
; GENERAL INFORMATION:
; APPLICANT: Schwiientek, Tilo
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: UPD-N-Acetylglucosamine:
; TITLE OF INVENTION: Galactose-beta1,3-N-Acetylglactosamine-alpha-R / (GlcNAc
; TITLE OF INVENTION: to GalNAc) beta1,6-N-Acetylglucosaminyltransferase, C2GnT3
; FILE REFERENCE: 4503/1G031
; CURRENT APPLICATION NUMBER: US/10/388,307
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US/09/645,192
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/150,488
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-388-307-11
```

```
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
```

US-09-966-880A-8 (1-198) x US-10-388-307-11 (1-20)

```
QY 125 GlyLeuArgArgLeu 129
Db 18 GGGTTGAGGAGACTG 4
```

#### RESULT 184

```
US-10-419-341-16
; Sequence 16, Application US/10419341
; Publication No. US20030180785A1
; GENERAL INFORMATION:
; APPLICANT: Krishnan, Rajendra
; APPLICANT: Coleman, Rebecca A.
; APPLICANT: Yoder, Christine C.
; APPLICANT: Dartschi, Becky A.
; APPLICANT: Brake, David
; TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULES ENCODING NEOSPORA PROTEINS
; FILE REFERENCE: PC9943A
; CURRENT APPLICATION NUMBER: US/10/419,341
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/276,438
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/079,389
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/112,282
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Neospora caninum
US-10-419-341-16
```

```
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
```

US-09-966-880A-8 (1-198) x US-10-419-341-16 (1-20)

```
QY 39 AlaThrSerPheSer 43
Db 4 GCGACTTCTTTTCT 18
```

#### RESULT 185

```
US-10-032-585-4132/c
; Sequence 4132, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4132
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4132

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-032-585-4132 (1-20)

Qy 22 LysGlyArgGlu 26
Db 19 AAGGCGAGGAGGAA 5

RESULT 186
US-10-032-585-5401/c
; Sequence 5401, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 0182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5401
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5401

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-032-585-5401 (1-20)

Qy 43 SerLeuArgPheGly 47
Db 16 AGCCITGACTCGGG 2

RESULT 187
US-10-109-349A-8
; Sequence 8, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REA
; TITLE OF INVENTION: METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL SAM
; FILE REFERENCE: 01154/2001-203
; CURRENT APPLICATION NUMBER: US/10/109,349A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-10-109-349A-8

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-109-349A-8 (1-20)

Qy 38 SerAlaThrSerPhe 42
Db 1 TCAGCAACCTCTTTC 15

RESULT 188
US-10-109-349A-262
; Sequence 262, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN R
; FILE REFERENCE: 01154/2001-203
; CURRENT APPLICATION NUMBER: US/10/109,349A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-109-349A-262

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-109-349A-262 (1-20)

Qy 19 ArgTTPAlaLysGly 23
Db 1 AGGTGGGCAAGGGA 15

RESULT 189
US-10-170-172-7/c
; Sequence 7, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: (20)
; OTHER INFORMATION: Synthesized with U at 3' terminus to provide
; OTHER INFORMATION: ribonucleic acid base for reactivity
US-10-170-172-7

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-7 (1-20)

Qy 56 HisValGluLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 190
US-10-408-085-59
; Sequence 59, Application US/10408085
; Publication No. US20030198989A1
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/408,085
; FILING DATE: 03-Apr-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/037,986
; FILING DATE: 18-Oct-2001
; APPLICATION NUMBER: 09/143,190
; FILING DATE: August 27, 1998
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
```

```
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-408-085-59

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-408-085-59 (1-20)

Qy 32 ValVallyeArgArg 36
Db 4 GTTGTAAACGACGG 18

RESULT 191
US-10-380-931-5
; Sequence 5, Application US/10380931
; Publication No. US20030215944A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTSP-0187
; CURRENT APPLICATION NUMBER: US/10/380,931
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/676,610
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-931-5

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-380-931-5 (1-20)

Qy 129 LeuHisArgAlaGly 133
Db 6 TTGCACAGGCGCAGG 20

RESULT 192
US-10-126-685-104/c
; Sequence 104, Application US/10126685
; Publication No. US20030219722A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20030219722A1e1
```

; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Broadway and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/126,685  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/009,319  
; FILING DATE: 1993-01-26  
; APPLICATION NUMBER: 07/664,989  
; FILING DATE: 01-MAR-1991  
; APPLICATION NUMBER: PCT/US89/03731  
; FILING DATE: 01-SEP-1989  
; APPLICATION NUMBER: 07/487,063  
; FILING DATE: 02-MAR-1990  
; APPLICATION NUMBER: 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28005  
; REFERENCE/DOCKET NUMBER: LADNER 7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: genomic DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
US-10-126-685-104

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-126-685-104 (1-20)

QY 178 ArgilleLeuPro 182  
Db 18 CGGATCCTCCTCCCT 4

## RESULT 193

US-10-236-031B-89/c  
; Sequence 89, Application US/10236031B  
; Publication No. US20030219760A1  
; GENERAL INFORMATION:  
; APPLICANT: Gordon, Gavin J.  
; APPLICANT: Jensen, Roderick V.  
; APPLICANT: Gullans, Steven R.  
; APPLICANT: Bueno, Raphael  
; TITLE OF INVENTION: Diagnostic and Prognostic Tests  
; FILE REFERENCE: B00801/70265 (JRV/JAV)  
; CURRENT APPLICATION NUMBER: US/10/236,031B

; CURRENT FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/317,389  
; PRIOR FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: US 60/407,431  
; PRIOR FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 89  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-236-031B-89  
Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-236-031B-89 (1-20)

QY 117 GluAspArgLysAla 121  
Db 17 GAAGACCGAAGGCT 3

## RESULT 194

US-10-174-771-30/c  
; Sequence 30, Application US/10174771  
; Publication No. US2003023034A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF JUNCTIONAL ADHESION MOLECULE 3 EXPRESSI  
; FILE REFERENCE: RTS-0430  
; CURRENT APPLICATION NUMBER: US/10/174,771  
; CURRENT FILING DATE: 2002-06-17  
; NUMBER OF SEQ ID NOS: 151  
; SEQ ID NO 30  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-174-771-30

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-771-30 (1-20)

QY 35 ArgArgAspSerAla 39  
Db 17 CGGAGAGACTCAGCC 3

## RESULT 195

US-10-174-771-101  
; Sequence 101, Application US/10174771  
; Publication No. US2003023034A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF JUNCTIONAL ADHESION MOLECULE 3 EXPRESSI  
; FILE REFERENCE: RTS-0430  
; CURRENT APPLICATION NUMBER: US/10/174,771  
; CURRENT FILING DATE: 2002-06-17  
; NUMBER OF SEQ ID NOS: 151  
; SEQ ID NO 101  
; LENGTH: 20

; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-174-771-101

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-771-101 (1-20)

QY 35 ArgAsgAspSerAla 39  
DB 4 CGGAGAGACTCAGCC 18

## RESULT 196

; Sequence 33, Application US/10176277  
; Publication No. US20030232443A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION  
; FILE REFERENCE: HTS-0022  
; CURRENT APPLICATION NUMBER: US/10/176,277  
; CURRENT FILING DATE: 2002-06-18  
; NUMBER OF SEQ ID NOS: 77  
; SEQ ID NO 33  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide

## US-10-176-277-33

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-176-277-33 (1-20)

QY 35 ArgAsgAspSerAla 39  
DB 1 CGGAGAGACTCAGCA 15

## RESULT 197

; Sequence 65, Application US/10176277  
; Publication No. US20030232443A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION  
; FILE REFERENCE: HTS-0022  
; CURRENT APPLICATION NUMBER: US/10/176,277  
; CURRENT FILING DATE: 2002-06-18  
; NUMBER OF SEQ ID NOS: 77  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-176-277-65

## Alignment Scores:

Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-176-277-65 (1-20)

QY 35 ArgAsgAspSerAla 39  
DB 20 CGGAGAGACTCAGCA 6

## RESULT 198

; Sequence 25, Application US/10174559  
; Publication No. US20030232773A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DRAK1 EXPRESSION  
; FILE REFERENCE: PTS-0006  
; CURRENT APPLICATION NUMBER: US/10/174,559  
; CURRENT FILING DATE: 2002-06-17  
; NUMBER OF SEQ ID NOS: 112  
; SEQ ID NO 25  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide

## US-10-174-559-25

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-559-25 (1-20)

QY 40 ThrSerPheSerIeu 44  
DB 3 ACATCTTTCCTTA 17

## RESULT 199

; Sequence 104, Application US/10127028  
; Publication No. US20040005539A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsay  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20040005539A1el  
; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible



```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,028
; FILING DATE: 22-APR-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,319
; FILING DATE: 1993-01-26
; APPLICATION NUMBER: 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-028-104

```

```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-10-127-028-104 (1-20)

```

QY 178 ArgilleLeuLeupro 182
DB 18 CGGATCCCTCCCT 4

```

#### RESULT 200

```

US-10-190-366-185/c
; Sequence 185, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 185
; LENGTH: 20
; TYPE: DNA
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-185

```

```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

```

```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-10-190-366-185 (1-20)

```

QY 78 ValThrTrpPheThr 82
DB 20 GTCACATGGTTCACA 6

```

#### RESULT 201

```

US-10-190-366-378
; Sequence 378, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 378
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-190-366-378

```

```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-10-190-366-378 (1-20)

```

QY 78 ValThrTrpPheThr 82
DB 1 GTCACATGGTTCACA 15

```

#### RESULT 202

```

US-10-289-762-3206/c
; Sequence 3206, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3206
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3206

```

```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-10-289-762-3206 (1-20)

```
QY 169 SerValArgLeuSer 173
Db 19 TCCGTGAGACTCTCT 5

RESULT 203
US-10-289-762-3704/c
; Sequence 3704, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3704
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3704

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-3704 (1-20)

QY 103 AsnLeuSerLeuArg 107
Db 20 AACCTCTCTCTGAGG 6

RESULT 204
US-10-289-762-3731/c
; Sequence 3731, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3731
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3731

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-3731 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 16 TTGTCTCTGAGATC 2

RESULT 205
US-10-289-762-3975
; Sequence 3975, Application US/10289762
```

```
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3975
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3975

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-3975 (1-20)

QY 176 LeuArgArgIleLeu 180
Db 6 TTGAGGAGGATCCTG 20

RESULT 206
US-10-289-762-4543
; Sequence 4543, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4543
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4543

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-4543 (1-20)

QY 111 AlaArgLeuTyrPhe 115
Db 2 GCCAGGCTGTATTTC 16

RESULT 207
US-10-289-762-4632/c
; Sequence 4632, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
```

; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4632

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-4632

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-4632 (1-20)

QY 179 IleLeuLeuProLeu 183

Db 20 ATTCTACTCCCTCTC 6

RESULT 208

US-10-289-762-4660/c

; Sequence 4660, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4660

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-4660

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-4660 (1-20)

QY 40 ThrSerPheSerLeu 44

Db 18 ACATCGTCTCCCTA 4

RESULT 209

US-10-289-762-5412/c

; Sequence 5412, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5412

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-5412

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-5412 (1-20)

QY 126 LeuArgLeuHis 130

Db 17 CTAAGCGGCTTACAT 3

RESULT 210

US-10-289-762-5709/c

; Sequence 5709, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5709

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-5709

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-5709 (1-20)

QY 104 LeuSerLeuArgile 108

Db 15 CTGCTCTCCGCATA 1

RESULT 211

US-10-289-762-6382/c

; Sequence 6382, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 6382

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-6382

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-6382 (1-20)

Qy 58 GluLeuPheLeu 62  
DB 20 GAGCTTCTCTTTTA 6

## RESULT 212

US-10-289-762-6501

; Sequence 6501, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 6501  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae

US-10-289-762-6501

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-6501 (1-20)

Qy 41 SerPheSerLeuAsp 45  
DB 5 AGTTTCTCTAGAC 19

## RESULT 213

US-10-188-777-88/C

; Sequence 88, Application US/10188777  
; Publication No. US20040006220A1  
; GENERAL INFORMATION:  
; APPLICANT: Sanjay Bhanot  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION  
; FILE REFERENCE: RTS-0358  
; CURRENT APPLICATION NUMBER: US/10/188,777  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 140  
; SEQ ID NO 88  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-188-777-88

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-777-88 (1-20)

Qy 170 ValArgLeuSerArg 174

DB 16 GTCCGCTCAGTCGC 2

## RESULT 214

US-10-188-777-137

; Sequence 137, Application US/10188777  
; Publication No. US20040006220A1  
; GENERAL INFORMATION:  
; APPLICANT: Sanjay Bhanot  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION  
; FILE REFERENCE: RTS-0358  
; CURRENT APPLICATION NUMBER: US/10/188,777  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 140  
; SEQ ID NO 137  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-188-777-137

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-777-137 (1-20)

Qy 170 ValArgLeuSerArg 174  
DB 5 GTCCGCTCAGTCGC 19

## RESULT 215

US-10-397-635-1

; Sequence 1, Application US/10397635  
; Publication No. US20040009604A1  
; GENERAL INFORMATION:  
; APPLICANT: ZHANG, XIAOLI  
; APPLICANT: FU, XUPING  
; TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER  
; TITLE OF INVENTION: THERAPY  
; FILE REFERENCE: P02410US2  
; CURRENT APPLICATION NUMBER: US/10/397,635  
; CURRENT FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 60/367,788  
; PRIOR FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 60/410,024  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-397-635-1

Alignment Scores:  
Pred. No.: 4.3e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-397-635-1 (1-20)

US-09-966-880A-8 (1-198) x US-10-126-544-104 (1-20)

D<sub>b</sub> 19 ACCTCCTGGTCACCA 5

```
RESULT 219
US-10-210-556-173
; Sequence 173, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTTPA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 173
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-210-556-173

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-210-556-173 (1-20)

QY 82 ThrSerTrpSerPro 86
| | | | | | | | | |
DB 2 ACCTCTGGTCACCA 16

RESULT 220
US-10-363-198-16
; Sequence 16, Application US/10363198
; Publication No. US20040023908A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/10/363,198
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 09/658,687
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-363-198-16

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-363-198-16 (1-20)

QY 107 ArgGlePheThrAla 111
| | | | | | | | | |
DB 1 CGTATCTTCACAGCT 15

RESULT 221
US-10-444-206-69
; Sequence 69, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-69

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-206-69 (1-20)

QY 176 LeuArgAcgIleIeu 180
| | | | | | | | | |
DB 1 CTGCGCCGAATCCTG 15

RESULT 222
US-10-444-206-166
; Sequence 166, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-166
```

```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-206-166 (1-20)

QY 176 LeuArgArgIleLeu 180
Db 2 CTGCGCGAATCTTG 16

RESULT 223
US-09-837-344-39/c
; Sequence 39, Application US/09837344
; Patent No. US20020041882A1
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,344
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 39: --
US-09-837-344-39

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-837-344-43 (1-12)

QY 59 LeuLeupheLeu 62
Db 12 TTGTTGTTCTTG 1

RESULT 224
US-09-837-344-43/c
; Sequence 43, Application US/09837344
; Patent No. US20020041882A1
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,344
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-837-344-43

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-837-344-43 (1-12)

QY 59 LeuLeupheLeu 62
Db 12 TTGTTGTTCTTG 1

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```
RESULT 225
US-09-835-370-54
; Sequence 54, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
; APPLICANT: UELMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of pna derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-54

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-835-370-54 (1-12)

QY 82 ThrSerTyrSer 85
Db 1 ACATCATGTCG 12

RESULT 226
US-09-875-453-18
; Sequence 18, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135.30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-09-875-453-18

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
```

```
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-875-453-18 (1-12)

QY 194 ArgThrLeuGly 197
Db 1 AGGACTCTTGGA 12

RESULT 227
US-09-900-112-56/c
; Sequence 56, Application US/09900112
; Publication No. US20030082209A1
; GENERAL INFORMATION:
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Schmidt, Alexander C.
; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vacci
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Parainfluenza Virus
US-09-900-112-56

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-900-112-56 (1-12)

QY 169 SerValArgLeu 172
Db 12 TCGTAGCTCTT 1

RESULT 228
US-09-900-112-60/c
; Sequence 60, Application US/09900112
; Publication No. US20030082209A1
; GENERAL INFORMATION:
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Schmidt, Alexander C.
; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vacci
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```



OTHER INFORMATION: Parainfluenza Virus  
US-09-900-112-60

Alignment Scores:  
Pred. No.: 12  
Score: 3.07e+04 Length: 12  
Matches: 4  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.02%  
DB: 10  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-900-112-60 (1-12)

QY 169 SerValArgLeu 172  
DB 12 TCCGTACGTCTA 1

RESULT 229

US-09-993-972C-852/c  
; Sequence 852, Application US/0903972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 852:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 852:

US-09-993-972C-852  
Alignment Scores:  
Pred. No.: 12  
Score: 3.07e+04 Length: 12  
Matches: 4

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.02%  
DB: 10  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-852 (1-12)

QY 90 CysAlaArgHis 93  
DB 12 TGTGCCGCCAT 1

RESULT 230

US-09-793-146-38  
; Sequence 38, Application US/09793146  
; Publication No. US20030203359A1  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, EUGEN  
; APPLICANT: BREIPOHL, GERHARD  
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR  
; PREPARATION AND USE  
; FILE REFERENCE: 02481.1437-02  
; CURRENT APPLICATION NUMBER: US/09/793,146  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: P 44 08 528.1  
; PRIOR FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: 08/402,838  
; PRIOR FILING DATE: 1995-03-13  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA  
US-09-793-146-38

Alignment Scores:

Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 2.02%  
DB: 11  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-793-146-38 (1-12)

QY 82 ThrSerTrpSer 85  
DB 1 ACATCATGTCG 12

RESULT 231

US-09-793-146-48  
; Sequence 48, Application US/09793146  
; Publication No. US20030203359A1  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, EUGEN  
; APPLICANT: BREIPOHL, GERHARD  
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR  
; PREPARATION AND USE  
; FILE REFERENCE: 02481.1437-02  
; CURRENT APPLICATION NUMBER: US/09/793,146  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: P 44 08 528.1  
; PRIOR FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: 08/402,838  
; PRIOR FILING DATE: 1995-03-13  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-49

Alignment Scores:
Pred. No.:      3.07e+04      Length:      12
Score:          4.00         Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     2.02%       Indels:        0
DB:              11         Gaps:          0

US-09-966-880A-8 (1-198) x US-09-793-146-48 (1-12)

QY      82 ThrSerTrpSer 85
      |||||
Db      1 ACATCATGTCG 12

RESULT 232
US-09-793-146-49/c
; Sequence 49, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; FILE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-49

Alignment Scores:
Pred. No.:      3.07e+04      Length:      12
Score:          4.00         Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     2.02%       Indels:        0
DB:              11         Gaps:          0

US-09-966-880A-8 (1-198) x US-09-793-146-49 (1-12)

QY      82 ThrSerTrpSer 85
      |||||
Db      12 ACATCATGTCG 1

RESULT 233
US-10-193-451A-24
; Sequence 24, Application US/10193451A
; Publication No. US20030096269A1
; GENERAL INFORMATION:
; APPLICANT: CULLIS, CHRISTOPHER A.
; APPLICANT: RADEMAN, SAMANTHA
; APPLICANT: KUNERT, KARL
; TITLE OF INVENTION: METHOD FOR FINDING GENETIC MARKERS
; FILE REFERENCE: 028315600005
; CURRENT APPLICATION NUMBER: US/10/193,451A
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/292,646
; PRIOR FILING DATE: 1999-04-15
```

```
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: WordPerfect for Windows v. 7.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
US-10-193-451A-24

Alignment Scores:
Pred. No.:      3.07e+04      Length:      12
Score:          4.00         Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     2.02%       Indels:        0
DB:              14         Gaps:          0

US-09-966-880A-8 (1-198) x US-10-193-451A-24 (1-12)

QY      41 SerPheSerLeu 44
      |||||
Db      1 AGCTTCTCCCTC 12

RESULT 234
US-10-437-038-24
; Sequence 24, Application US/10437038
; Publication No. US20030228665A1
; GENERAL INFORMATION:
; APPLICANT: GAUTVIK, KAARE M.
; APPLICANT: ALESTROM, PETER
; APPLICANT: OYEN, TORDIS BEATE
; APPLICANT: GABRIELSEN, ODD STOKKE
; TITLE OF INVENTION: PRODUCTION OF HUMAN PARATHYROID HORMONE FROM MICROORGANISMS
; FILE REFERENCE: 016777/0550
; CURRENT APPLICATION NUMBER: US/10/437,038
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/10/359,091
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 08/463,222
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/340,664
; PRIOR FILING DATE: 1994-11-16
; PRIOR APPLICATION NUMBER: 08/087,471
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 07/821,478
; PRIOR FILING DATE: 1992-01-15
; PRIOR APPLICATION NUMBER: 07/404,970
; PRIOR FILING DATE: 1989-09-08
; PRIOR APPLICATION NUMBER: 07/393,851
; PRIOR FILING DATE: 1989-08-14
; PRIOR APPLICATION NUMBER: 06/921,684
; PRIOR FILING DATE: 1986-10-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-437-038-24

Alignment Scores:
Pred. No.:      3.07e+04      Length:      12
Score:          4.00         Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     2.02%       Indels:        0
```

DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-437-038-24 (1-12)

QY 41 SerPheSerLeu 44

Db 1 AGCTTCAGCCTC 12

RESULT 235

US-10-359-091-24  
 ; Sequence 24, Application US/10359091  
 ; Publication No. US2004000568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GAUTVIK, KAARE M.  
 ; APPLICANT: ALESTROM, PETER  
 ; APPLICANT: OYEN, TORDIS BEATE  
 ; APPLICANT: GABRIELSEN, ODD STOKKE  
 ; TITLE OF INVENTION: PRODUCTION OF HUMAN PARATHYROID HORMONE FROM MICROORGANISMS  
 ; FILE REFERENCE: 016777/0550  
 ; CURRENT APPLICATION NUMBER: US/10/359,091  
 ; CURRENT FILING DATE: 2003-02-06  
 ; PRIOR APPLICATION NUMBER: 08/463,222  
 ; PRIOR FILING DATE: 1995-06-05  
 ; PRIOR APPLICATION NUMBER: 08/340,664  
 ; PRIOR FILING DATE: 1994-11-16  
 ; PRIOR APPLICATION NUMBER: 08/087,471  
 ; PRIOR FILING DATE: 1993-07-02  
 ; PRIOR APPLICATION NUMBER: 07/821,478  
 ; PRIOR FILING DATE: 1992-01-15  
 ; PRIOR APPLICATION NUMBER: 07/404,970  
 ; PRIOR FILING DATE: 1989-09-08  
 ; PRIOR APPLICATION NUMBER: 07/393,851  
 ; PRIOR FILING DATE: 1989-08-14  
 ; PRIOR APPLICATION NUMBER: 06/921,684  
 ; PRIOR FILING DATE: 1986-10-22  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 24  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-359-091-24

Alignment Scores:  
 Pred. No.: 3.07e-04 Length: 12  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-359-091-24 (1-12)

QY 41 SerPheSerLeu 44

Db 1 AGCTTCAGCCTC 12

RESULT 236

US-10-422-050-66  
 ; Sequence 66, Application US/10422050  
 ; Publication No. US20040009510A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sirna Therapeutics, Inc.  
 ; APPLICANT: Seiwert, Scott  
 ; APPLICANT: Zinnen, Shawn  
 ; APPLICANT: Vaish, Narendra  
 ; APPLICANT: Jadhav, Vasant  
 ; APPLICANT: Kossen, Karl  
 ; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
 ; FILE REFERENCE: 700/013 (MHBH 00-816-M)

; CURRENT APPLICATION NUMBER: US/10/422,050  
 ; CURRENT FILING DATE: 2003-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: US 10/286,492  
 ; PRIOR FILING DATE: 2002-11-01  
 ; PRIOR APPLICATION NUMBER: US 10/283,858  
 ; PRIOR FILING DATE: 2002-10-30  
 ; PRIOR APPLICATION NUMBER: US 10/056,761  
 ; PRIOR FILING DATE: 2002-01-23  
 ; PRIOR APPLICATION NUMBER: US 09/992,160  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: US 09/877,526  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 09/800,594  
 ; PRIOR FILING DATE: 2001-03-06  
 ; PRIOR APPLICATION NUMBER: US 60/187,128  
 ; PRIOR FILING DATE: 2000-03-06  
 ; NUMBER OF SEQ ID NOS: 102  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO 66  
 ; LENGTH: 12  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
 US-10-422-050-66

Alignment Scores:  
 Pred. No.: 3.07e-04 Length: 12  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-66 (1-12)

QY 100 GlyAsnProAsn 103

Db 1 GGAAUCCAAAC 12

RESULT 237

US-10-422-050-68  
 ; Sequence 68, Application US/10422050  
 ; Publication No. US20040009510A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sirna Therapeutics, Inc.  
 ; APPLICANT: Seiwert, Scott  
 ; APPLICANT: Zinnen, Shawn  
 ; APPLICANT: Vaish, Narendra  
 ; APPLICANT: Jadhav, Vasant  
 ; APPLICANT: Kossen, Karl  
 ; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
 ; FILE REFERENCE: 700/013 (MHBH 00-816-M)  
 ; CURRENT APPLICATION NUMBER: US/10/422,050  
 ; CURRENT FILING DATE: 2003-04-23  
 ; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: US 10/286,492  
 ; PRIOR FILING DATE: 2002-11-01  
 ; PRIOR APPLICATION NUMBER: US 10/283,858  
 ; PRIOR FILING DATE: 2002-10-30  
 ; PRIOR APPLICATION NUMBER: US 10/056,761  
 ; PRIOR FILING DATE: 2002-01-23  
 ; PRIOR APPLICATION NUMBER: US 09/992,160  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: US 09/877,526  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 09/800,594  
 ; PRIOR FILING DATE: 2001-03-06  
 ; PRIOR APPLICATION NUMBER: US 60/187,128  
 ; PRIOR FILING DATE: 2000-03-06

; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 68  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-68

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-68 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 238  
US-10-422-050-71  
; Sequence 71, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
; FILE REFERENCE: 700/013 (MBHB 00-816-M)  
; CURRENT APPLICATION NUMBER: US/10/422,050  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 10/286,492  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 10/283,858  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: US 10/056,761  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/992,160  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 09/877,526  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/800,594  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 71  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-72

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-72 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 240  
US-10-422-050-73  
; Sequence 73, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 68  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-68

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-68 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 238  
US-10-422-050-71  
; Sequence 71, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
; FILE REFERENCE: 700/013 (MBHB 00-816-M)  
; CURRENT APPLICATION NUMBER: US/10/422,050  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 10/286,492  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 10/283,858  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: US 10/056,761  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/992,160  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 09/877,526  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/800,594  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 71  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-72

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-72 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 240  
US-10-422-050-73  
; Sequence 73, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

; FILE REFERENCE: 700/013 (MEHB 00-816-M)  
; CURRENT APPLICATION NUMBER: US 10/422,050  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 10/286,492  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 10/283,858  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: US 10/056,761  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/992,160  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 09/877,526  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/800,594  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 73  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-73

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-73 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 241  
US-10-422-050-74  
; Sequence 74, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
; FILE REFERENCE: 700/013 (MEHB 00-816-M)  
; CURRENT APPLICATION NUMBER: US 10/422,050  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 10/286,492  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 10/283,858  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: US 10/056,761  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/992,160  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 09/877,526  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/800,594  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-75

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 74  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-74

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-74 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

RESULT 242  
US-10-422-050-75  
; Sequence 75, Application US/10422050  
; Publication No. US20040009510A1  
; GENERAL INFORMATION:  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Vaish, Narendra  
; APPLICANT: Jadhav, Vasant  
; APPLICANT: Kossen, Karl  
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules  
; FILE REFERENCE: 700/013 (MEHB 00-816-M)  
; CURRENT APPLICATION NUMBER: US 10/422,050  
; CURRENT FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: PCT/US 02/35529  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 10/286,492  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 10/283,858  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: US 10/056,761  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/992,160  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 09/877,526  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/800,594  
; PRIOR FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule  
US-10-422-050-75

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-75 (1-12)

Qy 100 GlyAsnProAsn 103  
Db 1 GGAAAUCCAAC 12

## RESULT 243

US-08-866-279A-13  
; Sequence 13, Application US/08866279A  
; Publication No. US20020170076A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan DYMECKI  
; TITLE OF INVENTION: Use of Flp Recombinase in Mice  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/866,279A  
; FILING DATE: 30-MAY-1997  
; CLASSIFICATION: 800  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-866-279A-13

Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-08-866-279A-13 (1-13)

Qy 10 LysPheLeuTyr 13  
Db 2 AAGTTCCTATAC 13

## RESULT 244

US-09-864-785-3628/c  
; Sequence 3628, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: 400/022 (MEHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3628  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-3628

Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-09-864-785-3628 (1-13)

Qy 72 ProGlyARGCys 75

Db 12 CCAGGAGATGC 1

## RESULT 245

US-09-864-785-3657  
; Sequence 3657, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: 400/022 (MEHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3657  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-3657

Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-09-864-785-3657 (1-13)

Qy 59 LeuLeuPheLeu 62

Db 2 UUGCUCUCUUA 13

## RESULT 246

US-09-093-972C-840/c  
; Sequence 840, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nycs, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY (IBS) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 840:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 840:
US-09-093-972C-840
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-093-972C-840 (1-13)
QY 90 CysAlaArgHis 93
Db 13 TGTGCCCGCCAT 2
RESULT 247
US-09-093-972C-851/c
; Sequence 851, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 851:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 851:
US-09-093-972C-851
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-093-972C-851 (1-13)
QY 90 CysAlaArgHis 93
Db 12 TGTGCCCGCCAT 1
RESULT 248
US-10-357-567-58/c
; Sequence 58, Application US/10357567
; Publication No. US20040038382A1
; GENERAL INFORMATION:
; APPLICANT: Coehigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-07748
; CURRENT APPLICATION NUMBER: US/10/357,567
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/046,845
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 58
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-357-567-58
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 2.02% Indels: 0  
DB: 12 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-357-567-58 (1-13)  
QY 195 ThrLeuGlyLeu 198  
DB 13 ACACGAGGCTG 2  
RESULT 249  
US-10-005-956-877/C  
; Sequence 877, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 877  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-005-956-877  
Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-005-956-877 (1-13)  
QY 39 AlaThrSerPhe 42  
DB 12 GCCACGAGCTTC 1  
RESULT 250  
US-10-005-956-903/C  
; Sequence 903, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 903  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-005-956-903  
Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13

Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-005-956-903 (1-13)  
QY 39 AlaThrSerPhe 42  
DB 12 GCCACGAGCTTC 1  
RESULT 251  
US-10-156-433-1  
; Sequence 1, Application US/10156433  
; Publication No. US20030144489A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Bellon, Laurent  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts  
; FILE REFERENCE: MBH00-943-E (500.007)  
; CURRENT APPLICATION NUMBER: US/10/156,433  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: US 10/112,814  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 09/216,584  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 09/094,381  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: US 60/068,212  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: US 60/049,002  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-156-433-1  
Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-156-433-1 (1-13)  
QY 59 LeuLeuPheLeu 62  
DB 1 TTGCTTTTCCTC 12  
RESULT 252  
US-10-156-433-2  
; Sequence 2, Application US/10156433  
; Publication No. US20030144489A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Bellon, Laurent  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts  
; FILE REFERENCE: MBH00-943-E (500.007)  
; CURRENT APPLICATION NUMBER: US/10/156,433  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: US 10/112,814



;  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 09/216,584  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 09/094,381  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: US 60/068,212  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: US 60/049,002  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-156-433-2

Alignment Scores:  
Pred. No.: 3,31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-433-2 (1-13)

Qy 59 LeuLeuPheLeu 62  
Db 2 TTGCTTTCTC 13

RESULT 253  
US-10-156-433-13  
; Sequence 13, Application US/10156433  
; Publication No. US2003014489A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Bellon, Laurent  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts  
; FILE REFERENCE: MHB00-943-E (500.007)  
; CURRENT APPLICATION NUMBER: US/10/156,433  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: US 10/112,814  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 09/216,584  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 09/094,381  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: US 60/068,212  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: US 60/049,002  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-156-433-13

Alignment Scores:  
Pred. No.: 3,31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-433-13 (1-13)

Qy 70 LeuAspProGly 73  
Db 1 CTGGATCCAGG 12

RESULT 254  
US-10-104-025-8/c  
; Sequence 8, Application US/10104025  
; Publication No. US20030165876A1  
; GENERAL INFORMATION:  
; APPLICANT: AVENTIS PHARMA SA  
; APPLICANT: BLANCHE, Francis  
; APPLICANT: CAMERON, Beatrice  
; TITLE OF INVENTION: PROCESSES FOR PURIFYING AND FOR DETECTING TARGET DOUBLE-STRANDED  
; FILE REFERENCE: 03806.0546  
; CURRENT APPLICATION NUMBER: US/10/104,025  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US 60/285,272  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: FR 0103953  
; PRIOR FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-025-8

Alignment Scores:  
Pred. No.: 3,31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-104-025-8 (1-13)

Qy 180 LeuLeuProLeu 183  
Db 13 CTTCTTCCTCT 2

RESULT 255  
US-10-112-814-1  
; Sequence 1, Application US/10112814  
; Publication No. US20030170644A1  
; GENERAL INFORMATION:  
; APPLICANT: Alex, Burgin  
; APPLICANT: Leonid, Beigelman  
; APPLICANT: Laurent, Bellon  
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts  
; FILE REFERENCE: MHB00-943-D; 400.005  
; CURRENT APPLICATION NUMBER: US/10/112,814  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: 09/216,584  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 09/094,381  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: 60/068,212  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: 60/049,002  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Accessible site within Bcl-2 transcript  
US-10-112-814-1

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Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-1 (1-13)
QY 59 LeuLeuPheLeu 62
Db 1 TTGCTTTTCCTC 12

RESULT 256
US-10-112-814-2
; Sequence 2, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Ballon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-943-D; 400.005
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-2
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-2 (1-13)
QY 59 LeuLeuPheLeu 62
Db 2 TTGCTTTTCCTC 13

RESULT 257
US-10-112-814-13
; Sequence 13, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Ballon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-943-D; 400.005
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/216,584
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; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-13
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-13 (1-13)
QY 70 LeuAspProGly 73
Db 1 CTGGATCCAGGA 12

RESULT 258
US-10-190-312A-121
; Sequence 121, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FRT sequence
US-10-190-312A-121
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-190-312A-121 (1-13)
QY 10 LysPheLeuTyr 13
Db 2 AAGTTTCATAC 13

RESULT 259
US-10-148-521-15/c
```

; Sequence 15, Application US/10148521  
; Publication No. US20030221203A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Pittsburgh  
; APPLICANT: Lotze, Michael T.  
; APPLICANT: Agha-Mohammadi, Siamak T.  
; TITLE OF INVENTION: High Efficiency Regulatable Gene Expression System  
; FILE REFERENCE: 00791PCT  
; CURRENT APPLICATION NUMBER: US/10/148,521  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/237,633  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic linker forward oligonucleotide  
US-10-148-521-15

Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-148-521-15 (1-13)  
QY 188 AspLeuArgAsp 191  
Db 12 GACCTTAGGGAC 1

RESULT 260  
US-10-194-180A-6  
; Sequence 6, Application US/10194180A  
; Publication No. US20040009179A1  
; GENERAL INFORMATION:  
; APPLICANT: Kleven, Stanley H.  
; APPLICANT: Ferguson, Naola  
; TITLE OF INVENTION: Mycoplasma gallisepticum Formulation  
; FILE REFERENCE: 1700-002  
; CURRENT APPLICATION NUMBER: US/10/194,180A  
; CURRENT FILING DATE: 2002-07-13  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Mycoplasma gallisepticum  
US-10-194-180A-6

Alignment Scores:  
Pred. No.: 3.31e-04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-194-180A-6 (1-13)  
QY 33 ValIysArgArg 36  
Db 1 GTAAACACGCG 12

RESULT 261  
US-10-271-429A-4/c  
; Sequence 4, Application US/10271429A  
; Publication No. US20040023233A1

; GENERAL INFORMATION:  
; APPLICANT: Atherogenics, Inc.  
; TITLE OF INVENTION: Protection Against Oxidative Stress and Inflammation by a Cytop  
; TITLE OF INVENTION: Response Element  
; FILE REFERENCE: ATH118  
; CURRENT APPLICATION NUMBER: US/10/271,429A  
; CURRENT FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/329,870  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/329,870  
; PRIOR FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: human  
US-10-271-429A-4

Alignment Scores:  
Pred. No.: 3.31e+04 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-271-429A-4 (1-13)  
QY 38 SerAlaThrSer 41  
Db 13 TCTGCCACCTCA 2

RESULT 262  
US-08-591-486B-32  
; Sequence 32, Application US/08591486B  
; Publication No. US20020037866A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg F  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Gottingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition  
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Trea  
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,486B  
; FILING DATE: 11-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93111059.7  
; FILING DATE: 10-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/02218  
; FILING DATE: 6-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10496/P60122  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-9350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-591-486B-32

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-591-486B-32 (1-14)

QY 125 GlyLeuArgGag 128

DB 2 GGTGGCGTAGA 13

RESULT 263

US-09-504-231A-1373/C

; Sequence 1373, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1373

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1373

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-1373 (1-14)

QY 155 HisGluArgThr 158

DB 12 CATGAGCGGACC 1

; SEQ ID NO 1411  
; LENGTH: 14  
; TYPE: RNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1411

Alignment Scores:  
Pred. No.: 14  
Score: 3.54e+04  
Length: 14  
Matches: 4  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
DB: 9  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-1411 (1-14)

QY 42 PheSerLeuApp 45  
Db 2 UUCAGCUUGGAU 13

RESULT 266

US-09-504-231A-1469  
; Sequence 1469, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1469

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1469

Alignment Scores:  
Pred. No.: 14  
Score: 3.54e+04  
Length: 14  
Matches: 4  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
DB: 9  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-1469 (1-14)

QY 174 ArgGlnLeuArg 177  
Db 1 CGGACGCUCCGG 12

RESULT 267

US-09-804-700-8

; Sequence 8, Application US/09804700

; Patent No. US20020081594A1

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert D.

; APPLICANT: Caradonna, Salvatore J.

; TITLE OF INVENTION: Uracil DNA Metabolism As A Target For Chemotherapy:

; FILE REFERENCE: Screening Assays and Related Method

; FILE REFERENCE: UMDNJ SOM-00-06

; CURRENT APPLICATION NUMBER: US/09/804,700

; CURRENT FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: US 60/189,516

; PRIOR FILING DATE: 2000-03-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Saccharomyces cerevisiae synthetic oligonucleotide

US-09-804-700-8

Alignment Scores:

Pred. No.: 3.54e+04

Score: 4.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.02%

Indels: 0

DB: 9

Gaps: 0

US-09-966-880A-8 (1-198) x US-09-804-700-8 (1-14)

QY 128 ArgLeuHisArg 131

Db 2 CGCCTCCACCGC 13

RESULT 268

US-09-274-553D-1373/c

; Sequence 1373, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1373

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-1373

Alignment Scores:

Pred. No.: 3.54e+04

Score: 4.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.02%

Indels: 0

DB: 9

Gaps: 0

Length: 14

Matches: 4

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

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US-09-966-880A-8 (1-198) x US-09-274-553D-1373 (1-14)
QY 155 HisGluArgThr 158
Db 12 CATGAGCGGACC 1

RESULT 269
US-09-274-553D-1375
; Sequence 1375, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1375
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1375

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-274-553D-1375 (1-14)
QY 110 ThrAlaArgLeu 113
Db 3 ACUGCCGUCUC 14

RESULT 270
US-09-274-553D-1411
; Sequence 1411, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1411
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1411

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-274-553D-1411 (1-14)
QY 42 PheSerLeuArg 45
Db 2 UUCAGCUUGGAU 13

RESULT 271
US-09-274-553D-1469
; Sequence 1469, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1469
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1469

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-274-553D-1469 (1-14)
QY 174 ArgGlnLeuArg 177
Db 1 CCGCAGCUCGCG 12

RESULT 272
US-09-931-184-1
; Sequence 1, Application US/09931184
; Patent No. US20020119095A1
; GENERAL INFORMATION:
```

; APPLICANT: Gabathuler, Reinhard  
 ; APPLICANT: Kolaitis, Gerrassimos  
 ; APPLICANT: Brooks, Robert  
 ; APPLICANT: Chen, Qingqi  
 ; APPLICANT: Karkan, Delara  
 ; APPLICANT: Arthur, Gavin  
 ; APPLICANT: St. Pierre, Jean Paul  
 ; APPLICANT: Jeffries, Wilfred  
 ; APPLICANT: Vitalis, Timothy  
 ; TITLE OF INVENTION: Chemotherapeutic Agents Conjugated to p97 and Their Methods of Use  
 ; FILE REFERENCE: 7685-47  
 ; CURRENT APPLICATION NUMBER: US/09/931,184  
 ; CURRENT FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: US 60/226,254  
 ; PRIOR FILING DATE: 2000-08-17  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 14  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-09-931-184-1

Alignment Scores:  
 Pred. No.: 3.54e+04 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-931-184-1 (1-14)

Qy 95 AlaAppHeu 98  
 Db 1 GCGGACTTCCTC 12

RESULT 273

US-09-915-063-2/c  
 ; Sequence 2, Application US/09915063  
 ; Publication No. US20030082544A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fors, Lance  
 ; APPLICANT: Ganske, Rocky  
 ; TITLE OF INVENTION: Methods and Systems for Validating Detection Assays, Developing I  
 ; TITLE OF INVENTION: Diagnostic DNA or RNA Analysis Products, and Increasing Revenue  
 ; TITLE OF INVENTION: Margins from In-Vitro Diagnostic DNA or RNA Analysis Assays  
 ; FILE REFERENCE: FORS-06467  
 ; CURRENT APPLICATION NUMBER: US/09/915,063  
 ; CURRENT FILING DATE: 2001-07-21  
 ; PRIOR APPLICATION NUMBER: 60/304,521  
 ; PRIOR FILING DATE: 2001-07-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 14  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-09-915-063-2

Alignment Scores:  
 Pred. No.: 3.54e+04 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-915-063-2 (1-14)  
 Qy 38 SerAlaThrSer 41  
 Db 13 TGTGCCACGTCA 2  
 RESULT 274  
 US-09-972C-827/c  
 ; Sequence 827, Application US/09093972C  
 ; Publication No. US20030087845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nyce, Jonathan W.  
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
 ; BRONCHIOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
 ; NUMBER OF SEQUENCES: 996  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
 ; STREET: 7 Clarke Drive  
 ; CITY: Cranbury  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 08512  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/093,972C  
 ; FILING DATE: 09-Jun-1998  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/472,527  
 ; FILING DATE: 7-June-1995  
 ; APPLICATION NUMBER: US 08/757,024  
 ; FILING DATE: 26-11-1996  
 ; APPLICATION NUMBER: US 08/472,527  
 ; FILING DATE: 7-June-1995  
 ; APPLICATION NUMBER: US 09/016,464  
 ; FILING DATE: 30-January-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Amzel, Viviana  
 ; REGISTRATION NUMBER: 30,930  
 ; REFERENCE/DOCKET NUMBER: EPI-00672  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 609-409-3035  
 ; TELEFAX: 413-254-9245  
 ; TELEX: <Unknown>  
 ; INFORMATION FOR SEQ ID NO: 827:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 827:  
 US-09-093-972C-827  
 Alignment Scores:  
 Pred. No.: 3.54e+04 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-966-880A-8 (1-198) x US-09-093-972C-827 (1-14)  
 Qy 90 CysAlaArgHis 93  
 Db 14 TGTGCCCGCAT 3

## RESULT 275

US-09-093-972C-839/c  
; Sequence 839, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-June-1998  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 839:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 839:  
US-09-093-972C-839

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-839 (1-14)

Qy 90 CysAlaArGHIS 93

Db 13 TGTGCCCGCAT 2

## RESULT 276

US-09-972C-850/c  
; Sequence 850, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.

## ;

; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-June-1998  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 850:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 850:  
US-09-093-972C-850

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-850 (1-14)

Qy 90 CysAlaArGHIS 93

Db 12 TGTGCCCGCAT 1

## RESULT 277

US-09-929-135-2/c  
; Sequence 2, Application US/09929135  
; Publication No. US2003010470A1  
; GENERAL INFORMATION:  
; APPLICANT: Fors, Lance  
; APPLICANT: Ganske, Rocky  
; APPLICANT: Brower, Amy M.  
; APPLICANT: Ziarco, Witold M.  
; TITLE OF INVENTION: Electronic Medical Record, Library of Electronic Medical Record  
; TITLE OF INVENTION: Polymorphism Data, and Computer Systems and Methods for Use Th  
; FILE REFERENCE: FORS-06443



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; CURRENT APPLICATION NUMBER: US/09/929,135
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-929-135-2

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-929-135-2 (1-14)
QY 38 SerAlaThrSer 41
Db 13 TCTGCCACGTC A 2

RESULT 278
US-09-837-306-24
; Sequence 24, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-837-306-24

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-837-306-24 (1-14)
QY 169 SerValArgLeu 172
Db 3 TCAGTGAGACTC 14

RESULT 279
US-10-325-403-14/c
; Sequence 14, Application US/10325403
; Publication No. US20040033568A9
```

```
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TREATMENT OF DISEASES CAUSED
; BY EXPRESSION OF THE c-MYC
; GENE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION NUMBER: US/10/325,403
; FILING DATE: 23-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/936,422
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/241
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-325-403-14

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-325-403-14 (1-14)
QY 104 LeuSerLeuArg 107
Db 12 CTGCTTTGGCG 1

RESULT 280
US-10-133-642-4
; Sequence 4, Application US/10133642
; Publication No. US2003007693A1
; GENERAL INFORMATION:
; APPLICANT: Jeffries, Wilfred A.
; APPLICANT: McGeer, Patrick L.
; APPLICANT: Rothenberger, Sylvia
; APPLICANT: Food, Michael R.
; APPLICANT: Yamada, Tatsuo
; APPLICANT: Kennard, Malcolm
; TITLE OF INVENTION: Use of p97 and Iron Binding Proteins as Diagnostic and Therapeu
; FILE REFERENCE: 7685-48
```

; CURRENT APPLICATION NUMBER: US/10/133,642  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 09/285,040  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: US 08/520,933  
; PRIOR FILING DATE: 1995-08-31  
; PRIOR APPLICATION NUMBER: US 08/367,224  
; PRIOR FILING DATE: 1993-07-09  
; PRIOR APPLICATION NUMBER: PCT/CA93/00272  
; PRIOR FILING DATE: 1995-03-30  
; PRIOR APPLICATION NUMBER: US 07/912,291  
; PRIOR FILING DATE: 1992-07-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-133-642-4

Alignment Scores: 14  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-133-642-4 (1-14)

OY 95 AlaAspPheLeu 98  
Db 1 GCGGACTTCTC 12

## RESULT 281

US-10-291-230-45/c  
; Sequence 45, Application US/10291230  
; Publication No. US20030108939A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; APPLICANT: Chen, Zhidong  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678.US.A  
; CURRENT APPLICATION NUMBER: US/10/291,230  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing a  
; OTHER INFORMATION: n NruI site.  
US-10-291-230-45

Alignment Scores: 14  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0

DB: 14 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-291-230-45 (1-14)  
OY 171 ArgLeuSerArg 174  
Db 12 CGGCTCTCGGA 1

## RESULT 282

US-10-291-249-45/c  
; Sequence 45, Application US/10291249  
; Publication No. US20030119041A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; APPLICANT: Chen, Zhidong  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678.US.B  
; CURRENT APPLICATION NUMBER: US/10/291,249  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing  
; OTHER INFORMATION: n NruI site.  
US-10-291-249-45

Alignment Scores: 14  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-291-249-45 (1-14)

OY 171 ArgLeuSerArg 174  
Db 12 CGGCTCTCGGA 1

## RESULT 283

US-10-325-403-14/c  
; Sequence 14, Application US/10325403  
; Publication No. US20030162264A1  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TREATMENT OF DISEASES CAUSED  
; BY EXPRESSION OF THE c-MYC  
; GENE  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/325,403  
FILING DATE: 23-Dec-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/192,943  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/07/936,422  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 197/241  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-325-403-14

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-325-403-14 (1-14)

QY 104 LeuSerLeuArg 107  
Db 12 CTGCTTTGGGC 1

RESULT 284

US-10-353-751-2/c

; Sequence 2, Application US/10353751  
; Publication No. US20030219784A1  
; GENERAL INFORMATION:  
; APPLICANT: Ip, Hon S.  
; APPLICANT: Ziarro, Witold A.  
; APPLICANT: Donald, Glen  
; TITLE OF INVENTION: Systems and Methods for Analysis of Agricultural Products  
; FILE REFERENCE: FORS-07809  
; CURRENT APPLICATION NUMBER: US/10/353,751  
; CURRENT FILING DATE: 2003-01-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-353-751-2

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-353-751-2 (1-14)  
QY 38 SerAlaThrser 41  
Db 13 TCTGCCACGTCA 2

RESULT 285

US-10-045-674-24

; Sequence 24, Application US/10045674  
; Publication No. US20030232333A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, ROBERT C.  
; APPLICANT: COHEN, EDWARD H.  
; APPLICANT: NASTRI, HORACIO G.  
; APPLICANT: ROOKEY, KRISTIN L.  
; APPLICANT: HOET, RENE  
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.  
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: DVAX/002 CIP2  
; CURRENT APPLICATION NUMBER: US/10/045,674  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 60/198,069  
; PRIOR FILING DATE: 2000-04-17  
; PRIOR APPLICATION NUMBER: 09/837,306  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 635  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-045-674-24

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-045-674-24 (1-14)

QY 169 SerValArgLeu 172  
Db 3 TCACTGAGACTC 14

RESULT 286

US-10-321-039-754/c

; Sequence 754, Application US/10321039  
; Publication No. US20040014067A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Lukowiak, Andrew  
; APPLICANT: Jarvis, Nancy  
; APPLICANT: Kurensky, David  
; TITLE OF INVENTION: Amplification Methods and Compositions  
; FILE REFERENCE: FORS-06960  
; CURRENT APPLICATION NUMBER: US/10/321,039  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: 09/998,157  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/329,113  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/360,489  
; PRIOR FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 759  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 754  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-039-754

Alignment Scores:  
Pred. No.: 3.54e+04 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-321-039-754 (1-14)

QY 38 SerAlaThrSer 41  
Db 13 TCTGCCACGTCA 2

## RESULT 287

US-09-767-395-35  
; Sequence 35, Application US/09767395  
; Patent No. US2002004215A1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane K  
; Derbyshire, Elaine J  
; McCafferty, John G  
; Vaughan, Tristan J  
; Johnson, Kevin S

TITLE OF INVENTION: Labelling and selection of molecules  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/767,395  
FILING DATE: 23-Jan-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/098,244

FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/GB97/01835

FILING DATE: 08-JUL-1997

APPLICATION NUMBER: GB 9614292.2

FILING DATE: 08-JUL-1996

APPLICATION NUMBER: GB 9624880.2

FILING DATE: 29-NOV-1996

APPLICATION NUMBER: GB 9712818.5

FILING DATE: 18-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/34800

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-767-395-35

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-767-395-35 (1-15)

QY 83 SerTrpSerPro 86  
Db 4 TCCTGGAGCCG 15

## RESULT 288

US-09-504-231A-82  
; Sequence 82, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA

; FILE REFERENCE: Ipi 247/282 HEPATITIS C VIRUS INFECTION

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 82

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-82

Alignment Scores:

Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-82 (1-15)

QY 59 LeuLeuPheLeu 62  
Db 3 UUGCUCUUCUC 14

## RESULT 289

US-09-504-231A-197  
; Sequence 197, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 197  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-197

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-197 (1-15)

QY 164 GlyLeuHisGlu 167  
DB 3 GGCCUUCAGAA 14

## RESULT 290

US-09-504-231A-198  
; Sequence 198, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 198  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-198

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-198 (1-15)

QY 164 GlyLeuHisGlu 167  
DB 2 GGCCUUCAGAA 13

## RESULT 291

US-09-504-231A-246/c  
; Sequence 246, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 246  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-246

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-246 (1-15)

QY 72 ProGlyArgCys 75  
DB 15 CCCGGAAGATGC 4

## RESULT 292

US-09-504-231A-247/c  
; Sequence 247, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 247  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-247

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-247 (1-15)

QY 72 ProGlyArgCys 75  
|||  
DB 13 CCGGAAGATGC 2

RESULT 293

US-09-504-231A-248/c  
; Sequence 248, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 248  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-248

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-248 (1-15)

QY 72 ProGlyArgCys 75  
|||  
DB 12 CCGGAAGATGC 1

RESULT 294

US-09-504-231A-249  
; Sequence 249, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 249  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-249

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-249 (1-15)

QY 125 GlyLeuArgArg 128  
|||  
DB 4 GGGUUGCGAAGG 15

RESULT 295

US-09-504-231A-321/c  
; Sequence 321, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 321  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-321

Alignment Scores: Length: 15  
Pred. No.: 3.78e+04  
Score: 4.00  
Matches: 4  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-09-504-231A-321 (1-15)

Qy 123 ProGluGlyLeu 126  
Db 12 CCGAGGCGCTC 1

## RESULT 296

US-09-504-231A-369  
; Sequence 369, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 369  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-369

Alignment Scores: Length: 15  
Pred. No.: 3.78e+04  
Score: 4.00  
Matches: 4  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-09-504-231A-369 (1-15)

Qy 128 ArgLeuHisArg 131  
Db 128 CCGAGGCGCTC 1

Db 4 CGGUUGCACAGG 15

## RESULT 297

US-09-504-231A-481  
; Sequence 481, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 481  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-481

## Alignment Scores:

Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-481 (1-15)

Qy 2 AspSerLeuLeu 5

Db 4 GACUCACUCUCU 15

## RESULT 298

US-09-504-231A-549  
; Sequence 549, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: tpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 549  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-549

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-549 (1-15)

Qy 59 LeuLeuPheLeu 62  
|||||  
Db 1 UUGCUCUUCUC 12

## RESULT 299

US-09-504-231A-711  
; Sequence 711, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: IPI 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 711

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-711

Alignment Scores:  
Pred. No.: 3.78e+04 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-711 (1-15)

Qy 59 LeuLeuPheLeu 62  
|||||  
Db 3 UUGCUCUUCUCU 14

## RESULT 300

US-09-504-231A-712

; Sequence 712, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: IPI 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 712

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-712

Alignment Scores:

Pred. No.: 3.78e+04 Length: 15

Score: 4.00 Matches: 4

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.02% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-712 (1-15)

Qy 59 LeuLeuPheLeu 62

|||||

Db 2 UUGCUCUUCUCU 13

Search completed: March 5, 2004, 03:19:31

Job time : 358 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 5, 2004, 00:23:04 ; Search time 80 seconds  
(without alignments)  
1373.503 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198

Sequence: 1 MDSLLMNRKFLYQKXVRW.....ILLPLYEVDLDRDAFRTGL 198

Scoring table:

Oligo Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 348605

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q/cgn2\_1/USPTO.spool/US0966880/runat\_04032004\_083153\_22415/app\_query.fasta\_1.391  
-DB=issued Patents NA -QMT=fastap -SUFFIX=Oligo.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=20  
-USER=US0966880 @CGN\_1\_1\_69 @runat\_04032004\_083153\_22415 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	6	3.0	18	4	US-09-422-978-11764	Sequence 11764, A
2	6	3.0	19	4	US-09-422-978-7618	Sequence 7618, Ap
3	6	3.0	20	2	US-08-651-692-2	Sequence 2, Appli
4	6	3.0	20	4	US-09-907-843-27	Sequence 27, Appl
5	6	3.0	20	4	US-09-422-978-9310	Sequence 9310, Ap
6	6	3.0	20	4	US-09-188-452A-5376	Sequence 5376, Ap
7	5	2.5	15	4	US-09-081-646-727	Sequence 727, App
8	5	2.5	16	1	US-07-664-989B-101	Sequence 101, App
9	5	2.5	16	5	PCT-US94-06331A-20	Sequence 20, Appl
10	5	2.5	17	1	US-08-758-306-583	Sequence 583, App
11	5	2.5	17	1	US-08-758-306-585	Sequence 585, App
12	5	2.5	17	2	US-08-292-620A-1635	Sequence 1635, Ap

13	5	2.5	17	2	US-08-292-620A-1691	Sequence 1691, Ap
14	5	2.5	17	2	US-08-292-620A-1891	Sequence 1891, Ap
15	5	2.5	17	2	US-08-292-620A-1581	Sequence 1581, Ap
16	5	2.5	17	2	US-08-292-620A-1586	Sequence 1586, Ap
17	5	2.5	17	3	US-09-071-845-1635	Sequence 1635, Ap
18	5	2.5	17	3	US-09-071-845-1691	Sequence 1691, Ap
19	5	2.5	17	3	US-09-071-845-1891	Sequence 1891, Ap
20	5	2.5	17	3	US-09-071-845-1891	Sequence 1891, Ap
21	5	2.5	17	3	US-09-071-845-1896	Sequence 1896, Ap
22	5	2.5	17	4	US-08-584-040-2010	Sequence 2010, Ap
23	5	2.5	17	4	US-08-584-040-2011	Sequence 2011, Ap
24	5	2.5	17	4	US-08-584-040-4354	Sequence 4354, Ap
25	5	2.5	17	4	US-08-584-040-4355	Sequence 4355, Ap
26	5	2.5	17	4	US-08-584-040-4356	Sequence 4356, Ap
27	5	2.5	17	4	US-08-584-040-7303	Sequence 7303, Ap
28	5	2.5	17	4	US-08-584-040-7304	Sequence 7304, Ap
29	5	2.5	17	4	US-08-676-342A-31	Sequence 31, Appl
30	5	2.5	17	4	US-09-474-432B-346	Sequence 346, App
31	5	2.5	17	4	US-09-371-772B-555	Sequence 555, App
32	5	2.5	17	4	US-09-371-772B-556	Sequence 556, App
33	5	2.5	17	4	US-09-371-772B-2121	Sequence 2121, Ap
34	5	2.5	17	4	US-09-371-772B-2122	Sequence 2122, Ap
35	5	2.5	17	4	US-09-371-772B-2123	Sequence 2123, Ap
36	5	2.5	17	4	US-09-371-772B-3112	Sequence 3112, Ap
37	5	2.5	17	4	US-09-371-772B-3113	Sequence 3113, Ap
38	5	2.5	17	4	US-09-371-772B-4848	Sequence 4848, Ap
39	5	2.5	17	4	US-09-476-387-345	Sequence 345, App
40	5	2.5	17	4	US-09-866-108A-9581	Sequence 9581, Ap
41	5	2.5	17	4	US-09-866-108A-9582	Sequence 9582, Ap
42	5	2.5	17	4	US-09-866-108A-9583	Sequence 9583, Ap
43	5	2.5	17	4	US-09-866-108A-9630	Sequence 9630, Ap
44	5	2.5	17	4	US-09-866-108A-9631	Sequence 9631, Ap
45	5	2.5	17	4	US-09-866-108A-9632	Sequence 9632, Ap

#### ALIGNMENTS

RESULT 1  
US-09-422-978-11764  
; Sequence 11764, Application US/09422378  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/09/422, 978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298, 850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109, 732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082, 614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 11764  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..18  
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in complen  
US-09-422-978-11764

Alignment Scores:  
Pred. No.: 87.3 Length: 18  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.03% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-11764 (1-18)

Qy 179 ILeuLeuProLeuTyr 184  
Db 1 ATCCTTCTCCCACTTAC 18

## RESULT 2

US-09-422-978-7618/c  
; Sequence 7618, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET 020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; EARLIER FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 7618  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: upstream amplification primer 99-9709 for SEQ 3684,  
US-09-422-978-7618

## Alignment Scores:

Pred. No.:	92	Length:	19
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-422-978-7618 (1-19)

Qy 167 GluAsnSerValArgLeu 172  
Db 19 GAAATAGTGTAGGCTC 2

## RESULT 3

US-08-651-692-2  
; Sequence 2, Application US/08651692  
; Patent No. 5856099  
; GENERAL INFORMATION:  
; APPLICANT: Loren Miraglia, Thomas Geiger  
; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean  
; TITLE OF INVENTION: Compositions and Methods for  
; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Jane Massey Licata  
; STREET: 210 Lake Drive East, Suite 201  
; CITY: Cherry Hill  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/651,692  
; FILING DATE: Herewith  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 779-2400  
; TELEFAX: (609) 779-8488  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
US-08-651-692-2

Alignment Scores:	96.8	Length:	20
Pred. No.:	6.00	Matches:	6
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x US-08-651-692-2 (1-20)

Qy 125 GlyLeuArgArgLeuHis 130  
Db 2 GGGCTGCGCGCTCCAC 19

## RESULT 4

US-09-907-843-27/c  
; Sequence 27, Application US/09907843  
; Patent No. 6440739  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION  
; FILE REFERENCE: RTS-0279  
; CURRENT APPLICATION NUMBER: US/09/907,843  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 27  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-907-843-27

Alignment Scores:	96.8	Length:	20
Pred. No.:	6.00	Matches:	6
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-907-843-27 (1-20)

Qy 122 GluProGluGlyLeuArg 127  
Db 18 GAGCCTGAGGGCTGCGG 1

## RESULT 5

US-09-422-978-9310

```

; Sequence 9310, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENST.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20_bind
; OTHER INFORMATION: downstream amplification primer 99-24508 for SEQ 1445, in complement
US-09-422-978-9310

Alignment Scores:
Pred. No.: 96.8 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.03%
Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-9310 (1-20)

Qy 40 ThrSerPheSerLeuAsp 45
Db 2 ACAAGTTTCATAGAC 19

RESULT 6
US-09-198-452A-5376
; Sequence 5376, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5376
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5376

Alignment Scores:
Pred. No.: 96.8 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.03%
Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-5376 (1-20)

Qy 167 GluAsnSerValArgLeu 172
Db 1 GAGAACTCGGTGGCGCTG 18

```

```

RESULT 7
US-09-081-646-727
; Sequence 727, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and Cancer Cells
; FILE REFERENCE: 01107.74864
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 727
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-727

Alignment Scores:
Pred. No.: 839 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-081-646-727 (1-15)

Qy 93 HisValalaSphe 97
Db 1 CATGTGCTGACTTT 15

RESULT 8
US-07-664-989B-101
; Sequence 101, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989

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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/487,063  
;; FILING DATE: 02-MAR-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/240,160  
;; FILING DATE: 02-SEP-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Cooper, Iver P.  
;; REGISTRATION NUMBER: 28005  
;; REFERENCE/DOCKET NUMBER: LADNER 7  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; INFORMATION FOR SEQ ID NO: 101:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 base pairs  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: double  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: genomic DNA  
US-07-664-9898-101

Alignment Scores:  
Pred. No.: 894 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-664-989B-101 (1-16)

QY 178 ArcileuleuPro 182  
DB 1 CGGATCCTCCTCCCT 15

RESULT 9  
PCT-US94-06331A-20/c  
; Sequence 20, Application PC/TUS9406331A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF FIBROSIS AND  
; TITLE OF INVENTION: FIBROUS TISSUE DISEASE  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06331A  
; FILING DATE: June 2, 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

none

;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
PCT-US94-06331A-20

Alignment Scores:  
Pred. No.: 894 Length: 16  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-06331A-20 (1-16)

QY 21 Alalyaglyvargarg 25  
DB 15 GCATAGGTAGGAGG 1

RESULT 10  
US-08-758-306-583/c  
; Sequence 583, Application US/08758306  
; Patent No. 5807743  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH  
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
; NUMBER OF SEQUENCES: 1379  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/758,306  
; FILING DATE: December 3, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/132  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 583:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-758-306-583

Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-758-306-583 (1-17)

QY 124 GluglyLeuArg 128  
Db 17 GAAGGACTAAGAAGG 3

RESULT 11  
US-08-758-306-585/c  
; Sequence 585, Application US/08758306  
; Patent No. 5807743  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: McSwiggen, James A.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH  
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
; NUMBER OF SEQUENCES: 1379  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Fast-Seq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/758,306  
; FILING DATE: December 3, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/132  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 585:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-758-306-585  
Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-758-306-585 (1-17)

QY 124 GluglyLeuArg 128  
Db 16 GAAGGACTAAGAAGG 2

RESULT 12  
US-08-292-620A-1635  
; Sequence 1635, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1635:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-292-620A-1635

Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1635 (1-17)

QY 58 GluLeuPheLeu 62

two

Db 1 GAACUGCUCUCCUC 15

## RESULT 13

US-08-292-620A-1691

; Sequence 1691, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1691:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1691

## Alignment Scores:

Pred. No.:	949	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x US-08-292-620A-1691 (1-17)

Qy 58 GluLeuLeuPheLeu 62

Db 1 GAACUGCUCUCCUC 15

RESULT 15

## RESULT 14

US-08-292-620A-1891

; Sequence 1891, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1891:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1891

## Alignment Scores:

Pred. No.:	949	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x US-08-292-620A-1891 (1-17)

Qy 58 GluLeuLeuPheLeu 62

Db 1 GAACUGCUCUCCUC 15

RESULT 15

two

two

US-08-292-620A-1981  
; Sequence 1981, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1981:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-292-620A-1981

Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1981 (1-17)  
QY 58 GluLeuLeuPheLeu 62  
Db 1 GAACUGCUCUCCUC 15  
RESULT 16  
US-08-292-620A-1986  
; Sequence 1986, Application US/08292620A

Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1986:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-292-620A-1986

Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1986 (1-17)  
QY 58 GluLeuLeuPheLeu 62  
Db 1 GAACUGCUCUCCUC 15  
RESULT 17  
US-09-071-845-1635  
; Sequence 1635, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:

two

two

APPLICANT: Susan Grimm  
 APPLICANT: Dan T. Stinchcomb  
 APPLICANT: James McSwiggen  
 APPLICANT: Sean Sullivan  
 APPLICANT: Kenneth G. Draper  
 TITLE OF INVENTION: RIBOZYME TREATMENT OF  
 TITLE OF INVENTION: DISEASES OR CONDITIONS  
 TITLE OF INVENTION: RELATED TO LEVELS OF  
 TITLE OF INVENTION: INTRACELLULAR ADHESION  
 TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
 NUMBER OF SEQUENCES: 2390  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,845  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292,620  
 FILING DATE: August 17, 1994  
 APPLICATION NUMBER: 08/008,895  
 FILING DATE: January 19, 1993  
 APPLICATION NUMBER: 07/989,849  
 FILING DATE: December 7, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 208/149  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1635:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-071-845-1635

Alignment Scores: 949 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 3

US-09-966-880A-8 (1-198) x US-09-071-845-1635 (1-17)

QY 58 GluLeuLeuPheLeu 62  
 Db 1 GAACUGCUCUCCUC 15

RESULT 18

US-09-071-845-1691  
 ; Sequence 1691, Application US/09071845  
 ; Patent No. 6132967  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Susan Grimm  
 ; APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen  
 APPLICANT: Sean Sullivan  
 APPLICANT: Kenneth G. Draper  
 TITLE OF INVENTION: RIBOZYME TREATMENT OF  
 TITLE OF INVENTION: DISEASES OR CONDITIONS  
 TITLE OF INVENTION: RELATED TO LEVELS OF  
 TITLE OF INVENTION: INTRACELLULAR ADHESION  
 TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
 NUMBER OF SEQUENCES: 2390  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,845  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292,620  
 FILING DATE: August 17, 1994  
 APPLICATION NUMBER: 08/008,895  
 FILING DATE: January 19, 1993  
 APPLICATION NUMBER: 07/989,849  
 FILING DATE: December 7, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 208/149  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1691:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-071-845-1691

Alignment Scores: 949 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 3

US-09-966-880A-8 (1-198) x US-09-071-845-1691 (1-17)

QY 58 GluLeuLeuPheLeu 62  
 Db 1 GAACUGCUCUCCUC 15

RESULT 19

US-09-071-845-1891  
 ; Sequence 1891, Application US/09071845  
 ; Patent No. 6132967  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Susan Grimm  
 ; APPLICANT: Dan T. Stinchcomb  
 ; APPLICANT: James McSwiggen  
 ; APPLICANT: Sean Sullivan



```

; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1891:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1891

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1891 (1-17)

QY 58 GluLeuLeuPheLeu 62
Db 1 GAACGUCUCUCCUC 15

RESULT 20
US-09-071-845-1891
; Sequence 1891, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

```

; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1981

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1981 (1-17)

QY 58 GluLeuLeuPheLeu 62
Db 1 GAACGUCUCUCCUC 15

RESULT 21
US-09-071-845-1986
; Sequence 1986, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

; TITLE OF INVENTION: INTRACELLULAR ADHESION  
 ; TITLE OF INVENTION: MOLECULE-1 (1-CAM-1)  
 ; NUMBER OF SEQUENCES: 2390  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/071,845  
 ; FILING DATE: 1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/292,620  
 ; FILING DATE: August 17, 1994  
 ; APPLICATION NUMBER: 08/008,895  
 ; FILING DATE: January 19, 1993  
 ; APPLICATION NUMBER: 07/989,849  
 ; FILING DATE: December 7, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 208/149  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 1986:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-071-845-1986

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1986 (1-17)

QY 58 GluLeuLeuPheLeu 62  
 Db 1 GAACUGCUUUUUUCCUC 15

RESULT 22

; US-08-584-040-2010  
 ; Sequence 2010, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
 ; TITLE OF INVENTION: GROWTH FACTOR  
 ; NUMBER OF SEQUENCES: 8502

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/584,040  
 ; FILING DATE: January 11, 1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/005,974  
 ; FILING DATE: October 26, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 218/064  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 2010:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-584-040-2010

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-2010 (1-17)

QY 102 ProAsnLeuSerLeu 106  
 Db 3 CCGAUCUUCUUUG 17

RESULT 23

; US-08-584-040-2011  
 ; Sequence 2011, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
 ; TITLE OF INVENTION: GROWTH FACTOR  
 ; NUMBER OF SEQUENCES: 8502  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.

```
/
/
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2011:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-584-040-2011
/
/ Alignment Scores:
/ Pred. No.: 949 Length: 17
/ Score: 5.00 Matches: 5
/ Percent Similarity: 100.00% Conservative: 0
/ Best Local Similarity: 100.00% Mismatches: 0
/ Query Match: 2.53% Indels: 0
/ DB: 4 Gaps: 0
/
/ US-09-966-880A-8 (1-198) x US-08-584-040-2011 (1-17)
/
/ QY 102 ProAsnLeuSerLeu 106
/ DB 1 CCGAUAUCUUCUUG 15
/
/ RESULT 24
/ US-08-584-040-4354
/ Sequence 4354, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
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/
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 4354:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-584-040-4354
/
/ Alignment Scores:
/ Pred. No.: 949 Length: 17
/ Score: 5.00 Matches: 5
/ Percent Similarity: 100.00% Conservative: 0
/ Best Local Similarity: 100.00% Mismatches: 0
/ Query Match: 2.53% Indels: 0
/ DB: 4 Gaps: 0
/
/ US-09-966-880A-8 (1-198) x US-08-584-040-4354 (1-17)
/
/ QY 157 ArgThrPheLysAla 161
/ DB 3 AGAACUUUAAGCU 17
/
/ RESULT 25
/ US-08-584-040-4355
/ Sequence 4355, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
;
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 4355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-4355
;
Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-4355 (1-17)

QY 157 ArgThrPheLysAla 161
Db 2 AGAACUUUUAAGCU 16

RESULT 26
US-08-584-040-4356
; Sequence 4356, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

```

```

; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 4356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-4356
;
Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-4356 (1-17)

QY 157 ArgThrPheLysAla 161
Db 1 AGAACUUUUAAGCU 15

RESULT 27
US-08-584-040-7303
; Sequence 7303, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
;
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 7303:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

US-08-584-040-7303

Alignment Scores: 949 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 4

US-09-966-880A-8 (1-198) x US-08-584-040-7303 (1-17)

QY 179 IleLeuLeuProLeu 183

DB 2 AUAUCUUACCCUG 16

RESULT 28

US-08-584-040-7304  
 ; Sequence 7304, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
 ; TITLE OF INVENTION: GROWTH FACTOR  
 ; NUMBER OF SEQUENCES: 8502  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/584,040  
 ; FILING DATE: January 11, 1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/005,974  
 ; FILING DATE: October 26, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 218/064  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 7304:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-584-040-7304

Alignment Scores: 949 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00%

Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-7304 (1-17)

QY 179 IleLeuLeuProLeu 183

DB 1 AUAUCUUACCCUG 15

RESULT 29

US-08-676-342A-31/c  
 ; Sequence 31, Application US/08676342A  
 ; Patent No. 6348313  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIBSON, DAVID R.  
 ; TITLE OF INVENTION: Sequencing of Nucleic Acids  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
 ; STREET: 2200 Clarendon Blvd. Suite 1400  
 ; CITY: Arlington  
 ; STATE: VA  
 ; COUNTRY: US  
 ; ZIP: 22201  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: MS-DOS Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/676,342A  
 ; FILING DATE: 19-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB95/00109  
 ; FILING DATE: 20-JAN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9401200.2  
 ; FILING DATE: 21-JAN-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lebovitz, Richard M.  
 ; REGISTRATION NUMBER: 37,067  
 ; REFERENCE/DOCKET NUMBER: HLBB 4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-243-6333  
 ; TELEFAX: 703-243-6410  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 bases  
 ; TYPE: nucleotides  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-676-342A-31

Alignment Scores: 949 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 4

US-09-966-880A-8 (1-198) x US-08-676-342A-31 (1-17)

QY 104 LeuSerLeuArgile 108

DB 15 CTTTCACTCGAATT 1

RESULT 30

US-09-474-432B-346  
 ; Sequence 346, Application US/09474432B  
 ; Patent No. 6528640  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Burgin, Alex  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka  
 ; APPLICANT: Sweedler, David  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides  
 ; FILE REFERENCE: MBH00-831-B (247/276)  
 ; CURRENT APPLICATION NUMBER: US/09/474,432B  
 ; CURRENT FILING DATE: 1999-12-19  
 ; PRIOR APPLICATION NUMBER: US 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; PRIOR APPLICATION NUMBER: US 60/084,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: US 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: US 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; NUMBER OF SEQ ID NOS: 1526  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 346  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-09-474-432B-346

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Watch: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-474-432B-346 (1-17)

QY 89 AspCysalaarghis 93  
 DB 3 GAUUGGCGAGGCAC 17

RESULT 31  
 US-09-371-772B-555  
 ; Sequence 555, Application US/09371772B  
 ; Patent No. 6566127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Pavco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Growth of Endothelial Cells  
 ; FILE REFERENCE: MBH00,876-J (237/198)  
 ; CURRENT APPLICATION NUMBER: US/09/371,772B  
 ; CURRENT FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: US 60/005,974  
 ; PRIOR FILING DATE: 1995-10-26  
 ; PRIOR APPLICATION NUMBER: US 08/584,040  
 ; PRIOR FILING DATE: 1996-01-08  
 ; NUMBER OF SEQ ID NOS: 14225  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 555  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-09-371-772B-555

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2121

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

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US-09-966-880A-8 (1-198) x US-09-371-772B-2121 (1-17)

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QY 157 ArgThrPhelysala 161
Db 3 AGAACUUUAAGCU 17

```

RESULT 34

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US-09-371-772B-2122
; Sequence 2122, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2122

```

```

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-09-371-772B-2122 (1-17)

```

QY 157 ArgThrPhelysala 161
Db 2 AGAACUUUAAGCU 16

```

RESULT 35

```

US-09-371-772B-2123
; Sequence 2123, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B

```

```

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2123
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2123

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-09-371-772B-2123 (1-17)

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QY 157 ArgThrPhelysala 161
Db 1 AGAACUUUAAGCU 15

```

RESULT 36

```

US-09-371-772B-3112
; Sequence 3112, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3112
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3112

```

```

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

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US-09-966-880A-8 (1-198) x US-09-371-772B-3112 (1-17)

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QY 179 IleuleuProleu 183
Db 2 AUACUCUUAACCCUG 16

```

RESULT 37

```

US-09-371-772B-3113
; Sequence 3113, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:

```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Pavco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 ; FILE REFERENCE: MBH00,876-J (237/198)  
 ; CURRENT APPLICATION NUMBER: US/09/371,772B  
 ; CURRENT FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: US 60/005,974  
 ; PRIOR FILING DATE: 1995-10-26  
 ; PRIOR APPLICATION NUMBER: US 08/584,040  
 ; PRIOR FILING DATE: 1996-01-08  
 ; NUMBER OF SEQ ID NOS: 14225  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3113  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Mus sp.  
 US-09-371-772B-3113

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-3113 (1-17)

QY 179 ileLeuLeuProLeu 183  
 Db 1 AUACUUAUCCUUG 15

RESULT 38  
 US-09-371-772B-4848  
 ; Sequence 4848, Application US/09371772B  
 ; Patent No. 6566127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Pavco, Pam  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Stinchcomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 ; FILE REFERENCE: MBH00,876-J (237/198)  
 ; CURRENT APPLICATION NUMBER: US/09/371,772B  
 ; CURRENT FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: US 60/005,974  
 ; PRIOR FILING DATE: 1995-10-26  
 ; PRIOR APPLICATION NUMBER: US 08/584,040  
 ; PRIOR FILING DATE: 1996-01-08  
 ; NUMBER OF SEQ ID NOS: 14225  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4848  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-09-371-772B-4848

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-4848 (1-17)

QY 102 ProAsnLeuSerLeu 106  
 Db 2 CCGAUAUUAUUUG 16  
 RESULT 39  
 US-09-476-387-345  
 ; Sequence 345, Application US/09476387  
 ; Patent No. 6617438  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot  
 ; FILE REFERENCE: MBH00-831-C (243/073)  
 ; CURRENT APPLICATION NUMBER: US/09/476,387  
 ; CURRENT FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: 60/083,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; NUMBER OF SEQ ID NOS: 1524  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 345  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-09-476-387-345

Alignment Scores:  
 Pred. No.: 949 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-366-880A-8 (1-198) x US-09-476-387-345 (1-17)

QY 89 AspCysAlaArgHis 93  
 Db 3 GAUUGUGCGAGGCAC 17

RESULT 40  
 US-09-866-108A-9581/c  
 ; Sequence 9581, Application US/09866108A  
 ; Patent No. 6686188  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: Ji, Yonggang  
 ; APPLICANT: PENN, Sharon G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEOMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108A  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359



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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9581
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9581

Alignment Scores:
Pred. No.: 949          Length: 17
Score: 5.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9581 (1-17)

QY 41 SerPheSerLeuasp 45
DB 17 AGCTTTCCCTCGAC 3

RESULT 41
US-09-866-108A-9582/c
; Sequence 9582, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9581
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9581

Alignment Scores:
Pred. No.: 949          Length: 17
Score: 5.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9581 (1-17)

QY 41 SerPheSerLeuasp 45
DB 17 AGCTTTCCCTCGAC 3

RESULT 41
US-09-866-108A-9582/c
; Sequence 9582, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

```

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9582
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9582

Alignment Scores:
Pred. No.: 949          Length: 17
Score: 5.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9582 (1-17)

QY 41 SerPheSerLeuasp 45
DB 16 AGCTTTCCCTCGAC 2

RESULT 42
US-09-866-108A-9583/c
; Sequence 9583, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9583
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9583

Alignment Scores:

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Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9583 (1-17)

QY 41 SerPheSerLeuasp 45  
|||||  
DB 15 AGCTTTTCCCGAC 1

## RESULT 43

US-09-866-108A-9630  
; Sequence 9630, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aeomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 9630  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-9630  
Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9630 (1-17)

QY 124 GluclyLeuArg 128  
|||||  
DB 3 GAAGGGCTCCGAGG 17

Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9630 (1-17)

QY 124 GluclyLeuArg 128  
|||||  
DB 3 GAAGGGCTCCGAGG 17

## RESULT 44

US-09-866-108A-9631  
; Sequence 9631, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aeomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 9631  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-9631  
Alignment Scores:  
Pred. No.: 949 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9631 (1-17)

QY 124 GluclyLeuArg 128  
|||||  
DB 2 GAAGGGCTCCGAGG 16

## RESULT 45

US-09-866-108A-9632  
; Sequence 9632, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

```

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9765
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9765

Alignment Scores:
Pred. No.:          949
Score:              5.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:        2.53%
DB:                  4
Length:             17
Matches:             5
Conservative:        0
Mismatch:             0
Indels:               0
Gaps:                0

US-09-966-880A-8 (1-198) x US-09-866-108A-9765 (1-17)

QY      103 AnLeuSerLeuArg 107
      |||||
Db       3 AACCTCGCTGAGG 17

RESULT 47
US-09-866-108A-9766
; Sequence 9766, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

```

Patent No. 6686188  
 SEQ ID NO 9766  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-866-108A-9766

Alignment Scores:  
 Pred. No.: 949  
 Score: 5.00  
 Length: 17  
 Matches: 5  
 Percent Similarity: 100.00%  
 Conservativity: 0  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Query Match: 2.53%  
 Indels: 0  
 Gaps: 0  
 DB:

US-09-966-880A-8 (1-198) x US-09-866-108A-9766 (1-17)

QY 103 AsnLeuSerLeuArg 107  
 Db 2 AACCTCTCGTGAGG 16

RESULT 49  
 US-09-866-108A-9767  
 Sequence 9767, Application US/09866108A  
 Patent No. 6686188  
 GENERAL INFORMATION:

APPLICANT: GU, Yizhong  
 APPLICANT: JI, Yonggang  
 APPLICANT: PENN, Sharon G.  
 APPLICANT: HANZEL, David K.  
 APPLICANT: RANK, David R.  
 APPLICANT: CHEN, Wensheng  
 APPLICANT: SHANNON, Mark  
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 FILE REFERENCE: A6MICA-7  
 CURRENT APPLICATION NUMBER: US/09/866,108A  
 CURRENT FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 15755  
 SOFTWARE: A6MICA Sequence Listing Engine  
 Patent No. 6686188  
 SEQ ID NO 9767  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-866-108A-9767

Alignment Scores:  
 Pred. No.: 949  
 Score: 5.00  
 Length: 17  
 Matches: 5  
 Percent Similarity: 100.00%  
 Conservativity: 0  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Query Match: 2.53%  
 Indels: 0

DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x US-09-866-108A-9767 (1-17)  
 QY 103 AsnLeuSerLeuArg 107  
 Db 1 AACCTCTCGTGAGG 15

RESULT 49  
 US-07-977-284A-44  
 Sequence 44, Application US/07977284A  
 Patent No. 5558988  
 GENERAL INFORMATION:  
 APPLICANT: Prockop, Darwin J.  
 APPLICANT: Ala-Kokko, Leena  
 APPLICANT: Williams, Charlene J.  
 APPLICANT: Ritvaniemi, Pertti  
 APPLICANT: Baldwin, Clinton  
 APPLICANT: Hopkinson, Ian  
 APPLICANT: Ahmad, Nilofar Nina  
 TITLE OF INVENTION: METHODS OF DETECTING A GENETIC  
 TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS  
 NUMBER OF SEQUENCES: 261  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589888ris  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/977,284A  
 FILING DATE: 13-NOV-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TJU-0697  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 ANTI-SENSE: NO  
 US-07-977-284A-44

Alignment Scores:  
 Pred. No.: 1e+03  
 Score: 5.00  
 Length: 18  
 Matches: 5  
 Percent Similarity: 100.00%  
 Conservativity: 0  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Query Match: 2.53%  
 Indels: 0  
 Gaps: 0  
 DB:

US-09-966-880A-8 (1-198) x US-07-977-284A-44 (1-18)

QY 69 AspleuaspProgly 73  
 Db 3 GATCTGGATCTGGA 17

RESULT 50

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US-08-390-850-1123/c
; Sequence 1123, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600.
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-390-850-1123
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-390-850-1123 (1-18)
Qy 119 ArgLyAlaGluPro 123
Db 15 AGAAGCGGACCG 1
RESULT 51
; Sequence 1123, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela

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; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-1123
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-435-634-1123 (1-18)
Qy 119 ArgLyAlaGluPro 123
Db 15 AGAAGCGGACCG 1
RESULT 52
US-08-453-956-2
; Sequence 2, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY

```

STREET: 6300 COLUMBIA CENTER  
 CITY: SEATTLE  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/453,956  
 FILING DATE: 30-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/086,631  
 FILING DATE: July 1, 1993  
 APPLICATION NUMBER: US 07/938,331  
 FILING DATE: 28-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mcmasters, David D.  
 REGISTRATION NUMBER: 33,963  
 REFERENCE/DOCKET NUMBER: 990008.424C1  
 TELEPHONE: 206-622-4900  
 TELEFAX: 206-682-6031  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: ZC976  
 US-08-453-956-2

Alignment Scores:  
 Pred. No.: 1e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-453-956-2 (1-18)

QY 32 ValVallyeArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 53  
 US-08-086-631-2  
 Sequence 2, Application US/08086631  
 Patent No. 5776725  
 GENERAL INFORMATION:  
 APPLICANT: Kindsvogel, Wayne R.  
 TITLE OF INVENTION: GLUCAGON RECEPTORS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED AND BERRY  
 STREET: 6300 COLUMBIA CENTER  
 CITY: SEATTLE  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/086,631  
 FILING DATE: July 1, 1993

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/938,331  
 FILING DATE: 28-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mcmasters, David D.  
 REGISTRATION NUMBER: 33,963  
 REFERENCE/DOCKET NUMBER: 990008.424C1  
 TELEPHONE: 206-622-4900  
 TELEFAX: 206-682-6031  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: ZC976  
 US-08-086-631-2

Alignment Scores:  
 Pred. No.: 1e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-086-631-2 (1-18)

QY 32 ValVallyeArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 54  
 US-08-468-551-3  
 Sequence 3, Application US/08468551  
 Patent No. 5874212  
 GENERAL INFORMATION:  
 APPLICANT: Prockop, Darwin J.  
 APPLICANT: Rock, Matthew J.  
 APPLICANT: Garguly, Arupa  
 TITLE OF INVENTION: DETECTION OF SINGLE BASE MUTATIONS AND  
 TITLE OF INVENTION: OTHER VARIATIONS IN DOUBLE STRANDED DNA BY  
 TITLE OF INVENTION: CONFORMATION-SENSITIVE CELL ELECTROPHORESIS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
 STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
 STREET: FLOOR  
 CITY: PHILADELPHIA  
 STATE: PENNSYLVANIA  
 COUNTRY: UNITED STATES  
 ZIP: 19103-7086  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,551  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Doyle Leary Ph.D., Kathryn  
 REGISTRATION NUMBER: 36,317  
 REFERENCE/DOCKET NUMBER: 9855-5U1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-965-1284  
 TELEFAX: 215-567-2991  
 TELEX: 831-494  
 INFORMATION FOR SEQ ID NO: 3:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-551-3

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-468-551-3 (1-18)

QY 69 AspLeuAspProgly 73
Db 3 GATCTGGATCTTGGG 17

RESULT 55
US-08-532-727A-18/c
; Sequence 18, Application US/08532727A
; Patent No. 583239
; GENERAL INFORMATION:
; APPLICANT: ANDRIEN, MARC
; APPLICANT: DUPONT, ETIENNE
; APPLICANT: ROSSAU, RUDI
; APPLICANT: DECKANCK ILSE
; TITLE OF INVENTION: PROCESS FOR TYPING HLA-B USING SPECIFIC PRIMERS
; TITLE OF INVENTION: AND PROBES SETS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,727A
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Oligonucleotide Probe 12
; LOCATION: anneals to nucleotides 189-206 of exon 2 of HLA-
US-08-532-727A-18

Alignment Scores:
Pred. No.: 1e+03 Length: 18

```

```

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-532-727A-18 (1-18)

QY 112 ArgLeuTy-PheCys 116
Db 17 CGCTTGACTTCTGT 3

RESULT 56
US-08-452-930-2
; Sequence 2, Application US/08452930
; Patent No. 591635
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,930
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ZC976
US-08-452-930-2

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-452-930-2 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 57

```

US-08-256-426B-44  
; Sequence 44, Application US/08256426B  
; Patent No. 5948611  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; APPLICANT: Ala-Kokko, Leena  
; APPLICANT: Williams, Charlene J.  
; APPLICANT: Ritvaniemi, Pertti  
; APPLICANT: Baldwin, Clinton  
; APPLICANT: Hopkinson, Ian  
; APPLICANT: Ahmad, Nilofer Nina  
; TITLE OF INVENTION: Methods of Detecting A Genetic  
; CORRESPONDENCE ADDRESSES: 293  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 59486111ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,426B  
; FILING DATE: 03-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: PCT/US93/10964  
; FILING DATE: 12-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,284  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark Deluca  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1082  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; ANTI-SENSE: NO  
; US-08-256-426B-44

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x US-08-256-426B-44 (1-18)

Oy 69 AspleuaspProgly 73  
Db 3 GAICTGGAUCTTGA 17

RESULT 58

US-09-213-767-47/c  
; Sequence 47, Application US/09213767  
; Patent No. 5948680  
; GENERAL INFORMATION:  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION

; FILE REFERENCE: RTS-0024  
; CURRENT APPLICATION NUMBER: US/09/213,767  
; CURRENT FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 47  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-213-767-47

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x US-09-213-767-47 (1-18)

Oy 103 AsnLeuSerLeuArg 107  
Db 17 AACCTTCTCTCAGA 3

RESULT 59

US-09-205-144-10  
; Sequence 10, Application US/09205144  
; Patent No. 5958771  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESSION  
; FILE REFERENCE: RTS-0021  
; CURRENT APPLICATION NUMBER: US/09/205,144  
; CURRENT FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 10  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-205-144-10

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x US-09-205-144-10 (1-18)

Oy 59 LeuLeuPheLeuArg 63  
Db 4 CTATTATTCTTAGA 18

RESULT 60

US-09-205-144-42  
; Sequence 42, Application US/09205144  
; Patent No. 5958771  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESSION  
; FILE REFERENCE: RTS-0021  
; CURRENT APPLICATION NUMBER: US/09/205,144  
; CURRENT FILING DATE: 1998-12-03



```
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-921-13

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%    Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-205-921-13 (1-18)

QY 127 ArgArgLeuHisArg 131
Db 4 CGCGGCTCCACGC 18

RESULT 63
US-09-357-072-30/c
; Sequence 30, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-30

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%    Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-357-072-30 (1-18)

QY 43 SerLeuAspPheGly 47
Db 17 AGCCTGGACTTGTGT 3

RESULT 64
US-09-081-180-17
; Sequence 17, Application US/09081180
; Patent No. 6022847
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT:
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
```

```
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-144-42

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%    Indels: 0
DB: 2                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-205-144-42 (1-18)

QY 38 SerAlaThrSerPhe 42
Db 4 AGTGCTACCTCTTT 18

RESULT 61
US-09-211-631-19
; Sequence 19, Application US/09211631
; Patent No. 6001597
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; APPLICANT: Vanaja, Erica
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDES IN FICHA METHANOLICA
; FILE REFERENCE: 96-16C2
; CURRENT APPLICATION NUMBER: US/09/211,631
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-211-631-19

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%    Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-211-631-19 (1-18)

QY 32 ValValIysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 62
US-09-205-921-13
; Sequence 13, Application US/09205921A
; Patent No. 6008048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 18
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC976
; US-09-081-180-17
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-081-180-17 (1-18)
;
; QY 32 ValVallysAgtAgt 36
; DB 2 GTTGTAACGACGG 16
;
; RESULT 65
; US-09-040-786-17
; Sequence 17, Application US/09040786
; Patent No. 6025197
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,786
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
```

```
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC976
; US-09-040-786-17
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-040-786-17 (1-18)
;
; QY 32 ValVallysAgtAgt 36
; DB 2 GTTGTAACGACGG 16
;
; RESULT 66
; US-09-143-212-52/c
; Sequence 52, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Moria and Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-143-212-52
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-143-212-52 (1-18)
;
; QY 121 AlaGluProGluGly 125
; DB 16 GCTGAGCCTGAAGGA 2
;
; RESULT 67
; US-09-265-628-19
; Sequence 19, Application US/09265628
; Patent No. 6153424
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
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; APPLICANT: Vanaja, Erika
; TITLE OF INVENTION: PROTEASE-DEFICIENT STRAINS OF PICHIA
; FILE REFERENCE: 97-01C1
; CURRENT APPLICATION NUMBER: US/09/265,628
; CURRENT FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/152,180
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: US 60/058,822
; EARLIER FILING DATE: 1997-09-15
; EARLIER APPLICATION NUMBER: US 08/703,807
; EARLIER FILING DATE: 1996-08-26
; EARLIER APPLICATION NUMBER: US 60/042,910
; EARLIER FILING DATE: 1996-07-17
; EARLIER APPLICATION NUMBER: US 60/006,397
; EARLIER FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-265-628-19

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-265-628-19 (1-18)

Qy 32 ValValVyeArGArG 36
Db 2 GTGTAAACGACGG 16

RESULT 68
US-08-413-740A-172
; Sequence 172, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
```

```
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Botham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-413-740A-172

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-413-740A-172 (1-18)

Qy 125 GlyIeuArgArgLeu 129
Db 2 GGTCTACGGAGGCTC 16

RESULT 69
US-09-001-141-17
; Sequence 17, Application US/09001141
; Patent No. 6183953
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: CHROMOSOMAL MUTAGENESIS IN
; TITLE OF INVENTION: PICHIA METHANOLICA
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,141
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/058,822
; FILING DATE: 15-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 97-70
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
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```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ZC976
US-09-001-141-17

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00           Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%           Indels: 0
DB: 3                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-001-141-17 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 70
US-09-140-804-12
; Sequence 12, Application US/09140804
; Patent No. 6137930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-140-804-12

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00           Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%           Indels: 0
DB: 3                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-140-804-12 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 71
US-09-630-706-70/c
; Sequence 70, Application US/09630706
; Patent No. 627640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-70

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00           Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%           Indels: 0
DB: 3                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-630-706-70 (1-18)
Qy 186 ValAspAspLeuArg 190
Db 17 GTTGATGACCTTCGG 3

RESULT 72
US-09-522-217-77
; Sequence 77, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-522-217-77

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00           Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%           Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-522-217-77 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 73
US-09-653-403-20
; Sequence 20, Application US/09653403
; Patent No. 6348331
; GENERAL INFORMATION:

```

```

; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 2
; TITLE OF INVENTION: PROMOTER AND TERMINATOR
; FILE REFERENCE: 98-57
; CURRENT APPLICATION NUMBER: US/09/653,403
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-653-403-20

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-653-403-20 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTGTAAACGACGG 16

RESULT 74
US-09-294-531B-10
; Sequence 10, Application US/09294531B
; Patent No. 6372889
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Farrah, Theresa M.
; APPLICANT: Mauer, Mark F.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: SOLUBLE PROTEIN ZTMP0-1
; FILE REFERENCE: 97-67
; CURRENT APPLICATION NUMBER: US/09/294,531B
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,513
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-294-531B-10

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-294-531B-10 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTGTAAACGACGG 16

RESULT 75
US-09-434-408-12
; Sequence 12, Application US/09434408

```

```

; Patent No. 6440697
; GENERAL INFORMATION:
; APPLICANT: Venezia, Domenick
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
; FILE REFERENCE: 98-41
; CURRENT APPLICATION NUMBER: US/09/434,408
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 60/108,258
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-434-408-12

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-434-408-12 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTGTAAACGACGG 16

RESULT 76
US-10-013-784-20
; Sequence 20, Application US/10013784
; Patent No. 6440720
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE
; TITLE OF INVENTION: DEHYDROGENASE 2
; TITLE OF INVENTION: PROMOTER AND TERMINATOR
; FILE REFERENCE: 98-57
; CURRENT APPLICATION NUMBER: US/10/013,784
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/653,403
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-013-784-20

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-013-784-20 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTGTAAACGACGG 16

RESULT 77

```

US-08-171-384A-7/C  
; Sequence 7, Application US/08171384A  
; Patent No. 6475781  
; GENERAL INFORMATION:  
; APPLICANT: Mercola, Mark K.  
; APPLICANT: Deisinger, Prescott L.  
; APPLICANT: Stiles, Charles D.  
; TITLE OF INVENTION: TRANS-DOMINANT SUPPRESSOR GENES FOR  
; TITLE OF INVENTION: OLIGOMERIC PROTEINS  
; FILE REFERENCE: 00530-075001  
; CURRENT APPLICATION NUMBER: US/08/171.384A  
; CURRENT FILING DATE: 1993-12-21  
; PRIOR APPLICATION NUMBER: 07/846,972  
; PRIOR FILING DATE: 1992-03-06  
; PRIOR APPLICATION NUMBER: 07/525,245  
; PRIOR FILING DATE: 1990-05-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-08-171-384A-7

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-171-384A-7 (1-18)  
QY 59 LeuLeuphLeuArg 63  
DB 17 CTCTCTCTCTGCGA 3

RESULT 78  
US-09-153-242-8/C  
; Sequence 8, Application US/09153242  
; Patent No. 6482592  
; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim  
; APPLICANT: Uhlen, Mathias  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pUC18/pRIT28,  
; OTHER INFORMATION: forward, modulating module, generic  
US-09-153-242-8

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-153-242-8 (1-18)  
QY 32 ValVallysArg 36

DB 17 GTTGTAACGACGG 3

RESULT 79  
US-09-686-838B-12  
; Sequence 12, Application US/09686838B  
; Patent No. 6482612  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: Adipocyte-Specific Protein Homologs  
; FILE REFERENCE: 97-49D1  
; CURRENT APPLICATION NUMBER: US/09/686,838B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/140,804  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/056,983  
; PRIOR FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC976  
US-09-686-838B-12

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-686-838B-12 (1-18)  
QY 32 ValVallysArg 36  
DB 2 GTTGTAACGACGG 16

RESULT 80  
US-09-552-225A-19  
; Sequence 19, Application US/09552225A  
; Patent No. 6521233  
; GENERAL INFORMATION:  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Bishop, Paul  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3  
; FILE REFERENCE: 99-09  
; CURRENT APPLICATION NUMBER: US/09/552,225A  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/130,199  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC976  
US-09-552-225A-19

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-09-552-225A-19 (1-18)
QY 32 ValValLysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 81
US-09-585-228-28
; Sequence 28, Application US/09585228
; Patent No. 6531576
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Burkhead, Steven K.
; TITLE OF INVENTION: FOUR-HELICAL BUNDLE PROTEIN ZS1G81
; FILE REFERENCE: 99-13
; CURRENT APPLICATION NUMBER: US/09/585,228
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: US 60/137,057
; EARLIER FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC976
US-09-585-228-28

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-585-228-28 (1-18)
QY 32 ValValLysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 82
US-09-422-978-6619
; Sequence 619, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6619
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-14074 for SEQ 2685,
US-09-422-978-6619

```

```

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-6619 (1-18)
QY 102 ProAsnLeuSerLeu 106
Db 4 CCAATCTATCCCTC 18

RESULT 83
US-09-422-978-10343
; Sequence 10343, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in complen
US-09-422-978-10343

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-10343 (1-18)
QY 34 LysArgArgAspSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 84
US-09-404-641-6
; Sequence 6, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23

```

; PRIOR APPLICATION NUMBER: US 60/123,546  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/142,574  
; PRIOR FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-404-641-6

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-404-641-6 (1-18)

QY 32 ValvallysArgArg 36  
Db 2 GTGTAAACGACGG 16

RESULT 85  
US-09-923-246-77  
; Sequence 77, Application US/09923246  
; Patent No. 6605272  
; GENERAL INFORMATION:  
; APPLICANT: No. 6605272ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/923,246  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,504  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-923-246-77

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-923-246-77 (1-18)

QY 32 ValvallysArgArg 36  
Db 2 GTGTAAACGACGG 16

RESULT 86  
US-09-786-606-18  
; Sequence 18, Application US/09786606  
; Patent No. 6613547  
; GENERAL INFORMATION:  
; APPLICANT: ZymoGenetics, Inc.  
; APPLICANT: Raymond, Christopher K.  
; APPLICANT: Vanaja, Erica  
; APPLICANT: Miller, Brady G.  
; APPLICANT: Sloan, James S.  
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 1  
; FILE REFERENCE: 98-56PC  
; CURRENT APPLICATION NUMBER: US/09/786,606  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: US 60/140,703  
; PRIOR FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-09-786-606-18

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-786-606-18 (1-18)

QY 32 ValvallysArgArg 36  
Db 2 GTGTAAACGACGG 16

RESULT 87  
US-09-552-204A-19  
; Sequence 19, Application US/09552204A  
; Patent No. 6620909  
; GENERAL INFORMATION:  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACR2  
; FILE REFERENCE: 99-08  
; CURRENT APPLICATION NUMBER: US/09/552,204A  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/130,207  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC976  
US-09-552-204A-19  
Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0



Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-552-204A-19 (1-18)  
Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16  
RESULT 88  
US-10-295-723-77  
; Sequence 77, Application US/10295723  
; Patent No. 6686178  
; GENERAL INFORMATION:  
; APPLICANT: No. 6686178ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/295,723  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 09/522,217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,547  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; TYPE: DNA  
; LENGTH: 18  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer ZC976  
US-10-295-723-77  
Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0  
US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)  
Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16  
RESULT 89  
PCT-US93-08174-2  
; Sequence 2, Application PC/TUS9308174  
; GENERAL INFORMATION:  
; APPLICANT: NAME: ZymoGenetics, Inc.  
; APPLICANT: STREET: 4225 Roosevelt Way North East  
; APPLICANT: CITY: Seattle, Washington  
; APPLICANT: COUNTRY: United States  
; APPLICANT: POSTAL CODE: 98105  
; APPLICANT: TELEPHONE: (206) 547-80808  
; TITLE OF INVENTION: GLUCAGON RECEPTORS  
; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 COLUMBIA CENTER  
; CITY: SEATTLE  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 99104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08174  
; FILING DATE: 30-AUG-1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/086,631  
; FILING DATE: July 1, 1993  
; APPLICATION NUMBER: US 07/938,331  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 990008.424C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: ZC976  
PCT-US93-08174-2  
Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0  
US-09-966-880A-8 (1-198) x PCT-US93-08174-2 (1-18)  
Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16  
RESULT 90  
PCT-US95-04063-172  
; Sequence 172, Application PC/TUS9504063  
; GENERAL INFORMATION:  
; APPLICANT: HERNSTADT, CORINNA  
; APPLICANT: PARKER, WILLIAM D.  
; APPLICANT: DAVIS, ROBERT  
; APPLICANT: MILLER, SCOTT W.  
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and  
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial  
; TITLE OF INVENTION: Defects  
; NUMBER OF SEQUENCES: 206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenyon & Kenyon  
; STREET: 1025 Connecticut Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20036-5405  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04063  
FILING DATE: 30-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonham, David B.  
REGISTRATION NUMBER: 34297  
REFERENCE/DOCKET NUMBER: 2105/7  
TELEPHONE: (202) 429-1776  
TELEFAX: (202) 429-0796  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-04063-172

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x PCT-US95-04063-172 (1-18)

QY 125 GlyLeuArgLeu 129  
Db 2 GGTCTACGAGGCTC 16

RESULT 91  
5262866-10  
Patent No. 5262866  
APPLICANT: FRITSCH, EDWARD F.; COLLINS, MARY  
TITLE OF INVENTION: PROCESS AND NUCLEIC ACID CONSTRUCT FOR  
PRODUCING REAGENT COMPLEXES USEFUL IN DETERMINING TARGET  
NUCLEOTIDE SEQUENCES  
NUMBER OF SEQUENCES: 15  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/938,201  
FILING DATE: 11-APR-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 729,504  
FILING DATE: 02-MAY-1985  
APPLICATION NUMBER: 607,885  
FILING DATE: 07-MAY-1984  
APPLICATION NUMBER: 684,308  
FILING DATE: 20-DEC-1984  
APPLICATION NUMBER: 684,305  
FILING DATE: 20-DEC-1984  
APPLICATION NUMBER: 607,885  
FILING DATE: 07-MAY-1984  
SEQ ID NO: 10:  
LENGTH: 18  
5262866-10

Alignment Scores:  
Pred. No.: 1e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x 5262866-10 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAAAACGACGG 16

RESULT 92  
US-08-070-328A-17/C  
Sequence 17, Application US/08070328A  
Patent No. 5491225  
GENERAL INFORMATION:  
APPLICANT: Picone, Teresa  
APPLICANT: McCallum, Theresa  
APPLICANT: Zoccoli, Michael  
TITLE OF INVENTION: PCR PRIMERS FOR DETECTION OF  
LEGIONELLA SPECIES AND  
METHODS FOR CONTROLLING  
TITLE OF INVENTION: VISUAL INTENSITY IN NUCLEIC  
ACID HYBRIDIZATION ASSAYS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/070,328A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stas, Stacey R., Ph.D.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: 8784  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2863  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
US-08-070-328A-17

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x US-08-070-328A-17 (1-19)

QY 56 HisValGluLeu 60  
Db 18 CAGTAGACTGCTC 4

RESULT 93  
US-08-146-504-21  
Sequence 21, Application US/08146504  
Patent No. 5605662  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.; and Tu, Eugene  
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING

;; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR  
;; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND  
;; NUMBER OF SEQUENCES: 31  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 611 West Sixth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90017  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/146,504  
;; FILING DATE: No. 5605662ember 1, 1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; PRIOR APPLICATION DATA: including application  
;; PRIOR APPLICATION DATA: described below:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 203/218  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-146-504-21  
;;  
Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-146-504-21 (1-19)  
QY 56 HisValGluLeuLeu 60  
DB 2 CACGTAGACTGCTC 16  
RESULT 94  
US-08-455-116-17/c  
; Sequence 17, Application US/08455116  
; Patent No. 5614388  
; GENERAL INFORMATION:  
; APPLICANT: Picone, Teresa  
; APPLICANT: McCallum, Theresa  
; APPLICANT: Zoccoli, Michael  
; TITLE OF INVENTION: PCR PRIMERS FOR DETECTION OF LEGIONELLA  
; TITLE OF INVENTION: SPECIES AND METHODS FOR CONTROLLING VISUAL  
; TITLE OF INVENTION: INTENSITY IN NUCLEIC ACID HYBRIDIZATION  
; TITLE OF INVENTION: ASSAYS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey

;; COUNTRY: USA  
;; ZIP: 07110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.24  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/455,116  
;; FILING DATE: May 31, 1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Petty, Douglas A., Ph.D.  
;; REGISTRATION NUMBER: 35,321  
;; REFERENCE/DOCKET NUMBER: 9177  
;; TELEPHONE: (510) 814-2974  
;; TELEFAX: (510) 814-2977  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (probe)  
;; US-08-455-116-17  
;;  
Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-455-116-17 (1-19)  
QY 56 HisValGluLeuLeu 60  
DB 18 CACGTAGACTGCTC 4  
RESULT 95  
US-08-154-019-20  
; Sequence 20, Application US/08154019  
; Patent No. 5633076  
; GENERAL INFORMATION:  
; APPLICANT: Deboer, Herman A.  
; APPLICANT: Strijker, Rein  
; APPLICANT: Heyneker, Herbert L.  
; APPLICANT: Platenburg, Gerald  
; APPLICANT: Lee, Sang He  
; APPLICANT: Pieper, Frank  
; APPLICANT: Krimpenfort, Paul J.A.  
; TITLE OF INVENTION: Production of Recombinant Polypeptides  
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/154,019  
; FILING DATE: 16-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/461,333  
 FILING DATE: 05-JUN-1995  
 APPLICATION NUMBER: US 08/077,788  
 FILING DATE: 15-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/895,956  
 FILING DATE: 15-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/619,131  
 FILING DATE: 27-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/444,745  
 FILING DATE: 01-DEC-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Liebescheutz, Joe O.  
 REGISTRATION NUMBER: 37,505  
 REFERENCE/DOCKET NUMBER: 16994-003123  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-543-9600  
 TELEFAX: 415-543-5043  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-154-019-20

Alignment Scores:  
 Pred. No.: 1.06e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-154-019-20 (1-19)

Qy 32 ValVallyatqarg 36  
 Db 5 GTGTAAACGACGG 19

RESULT 96  
 US-08-634-331-15/c  
 Sequence 15, Application US/08634331  
 Patent No. 5707809  
 GENERAL INFORMATION:  
 APPLICANT: HALVERSON, Joy L.  
 APPLICANT: DVORAK, Jan  
 TITLE OF INVENTION: AVIAN SEX IDENTIFICATION PROBES  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/634,331  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SHERWOOD, Pamela J.  
 REGISTRATION NUMBER: 36,677  
 REFERENCE/DOCKET NUMBER: A-55362-3/BIR/PJS  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 494-8700  
 TELEFAX: (415) 494-8771  
 TELEX: 910 2777299FHT UR  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "Primer"  
 US-08-634-331-15  
 Alignment Scores:  
 Pred. No.: 1.06e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-966-880A-8 (1-198) x US-08-634-331-15 (1-19)  
 Qy 82 ThrSerTrrSerPro 86  
 Db 17 ACAAGCTGGAGCCCA 3  
 RESULT 97  
 US-08-295-743-18/c  
 Sequence 18, Application US/08295743  
 Patent No. 5719271  
 GENERAL INFORMATION:  
 APPLICANT: ISIS Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Covalently Cross-Linked  
 TITLE OF INVENTION: Oligonucleotides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
 ADDRESSEE: and No. 5719271ris  
 STREET: One Liberty Place - 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch disk, 720 Kb  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/295,743  
 FILING DATE: 30-AUG-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 846,376  
 FILING DATE: 05-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Joseph Lucci  
 REGISTRATION NUMBER: 33,307  
 REFERENCE/DOCKET NUMBER: ISIS-1006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-568-3100  
 TELEFAX: 215-568-3439  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 9  
 OTHER INFORMATION: 2'-O-[propion-3-yl bis(o-

OTHER INFORMATION: nitrobenzyl) acetal] group  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 17  
OTHER INFORMATION: 2'-O-[propion-3-al bis(o-  
OTHER INFORMATION: nitrobenzyl) acetal] group  
US-08-295-743-18

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880a-8 (1-198) x US-08-295-743-18 (1-19)

OY 179 IleLeuLeuProLeu 183

Db 17 ATTCTCTACTCTG 3

RESULT 98

US-08-461-333-20  
Sequence 20, Application US/08461333  
Patent No. 5741957  
GENERAL INFORMATION:  
APPLICANT: Deboer, Herman A.  
APPLICANT: Strijker, Rein  
APPLICANT: Heyneker, Herbert L.  
APPLICANT: Platenburg, Gerald  
APPLICANT: Lee, Sang He  
APPLICANT: Pieper, Frank  
APPLICANT: Krimpenfort, Paul J.A.  
TITLE OF INVENTION: Production of Recombinant Polypeptides  
TITLE OF INVENTION: by Bovine Species and Transgenic Methods  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,333  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,788  
FILING DATE: 15-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/895,956  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/619,131  
FILING DATE: 27-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/444,745  
FILING DATE: 01-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheutz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 16994-003123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-461-333-20

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880a-8 (1-198) x US-08-461-333-20 (1-19)

OY 32 ValVallysArgArg 36

Db 5 GTTGTAAACGACGG 19

RESULT 99

US-08-534-454-2  
Sequence 2, Application US/08534454  
Patent No. 5849486  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.; O'Connell, James P.; Juncosa, Robert D.; Soano  
TITLE OF INVENTION: APPARATUS AND METHODS FOR ACTIVE  
TITLE OF INVENTION: PROGRAMMABLE MATRIX DEVICES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: WINDOWS (VERSION 3.0)  
SOFTWARE: WordPerfect (Version 6.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/534,454  
FILING DATE: September 27, 1995  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/304,657  
FILING DATE: September 9, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, David B.  
REGISTRATION NUMBER: 31,125  
REFERENCE/DOCKET NUMBER: 216/054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-534-454-2

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-534-454-2 (1-19)

QY 56 HisValGluLeuLeu 60  
|||||

Db 2 CACGTAGAACTGCTC 16

## RESULT 100

US-08-725-976-21

; Sequence 21, Application US/08725976

; Patent No. 5929208

; GENERAL INFORMATION:

; APPLICANT: Heller, Michael J.; and Tu, Eugene

; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb

; COMPUTER: IBM compatible

; OPERATING SYSTEM: WINDOWS (VERSION 3.0)

; SOFTWARE: WordPerfect (Version 6.0)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/725,976

; FILING DATE: October 4, 1996

; CLASSIFICATION: 422

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/145,504

; FILING DATE: No. 5929208, September 1, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Murphy, David B.

; REGISTRATION NUMBER: 31,125

; REFERENCE/DOCKET NUMBER: 222/211

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 499-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-725-976-21

Alignment Scores:

Pred. No.: 1.06e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-725-976-21 (1-19)

QY 56 HisValGluLeuLeu 60  
|||||

Db 2 CACGTAGAACTGCTC 16

## RESULT 101

US-08-464-167-20

; Sequence 20, Application US/08464167

; Patent No. 6013857

; GENERAL INFORMATION:

; APPLICANT: Deboer, Herman A.

; APPLICANT: Strijker, Rein

; APPLICANT: Heyneker, Herbert L.  
; APPLICANT: Platenburg, Gerald  
; APPLICANT: Lee, Sang He  
; APPLICANT: Pieper, Frank  
; APPLICANT: Krampenfort, Paul J.A.  
; TITLE OF INVENTION: Production of Recombinant Polypeptides  
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods  
; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,167

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,788

; FILING DATE: 15-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/895,956

; FILING DATE: 15-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/619,131

; FILING DATE: 27-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/444,745

; FILING DATE: 01-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebescheutz, Joe O.

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 16994-003124

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-543-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-464-167-20

Alignment Scores:

Pred. No.: 1.06e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-464-167-20 (1-19)

QY 32 ValValLysArgArg 36  
|||||

Db 5 GTTGTAACGACGG 19

## RESULT 102

US-08-271-882B-21

; Sequence 21, Application US/08271882B

; Patent No. 6017696

; GENERAL INFORMATION:

; APPLICANT: Michael J. Heller

; APPLICANT: Eugene Tu

APPLICANT: Glen A. Evans  
APPLICANT: Ronald G. Sosnowski  
TITLE OF INVENTION: SELF-ADDRESSABLE  
TITLE OF INVENTION: SELF-ASSEMBLING  
TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND  
TITLE OF INVENTION: DEVICES FOR  
TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS  
TITLE OF INVENTION: AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/05/271,882B  
FILING DATE: July 7, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146,504  
FILING DATE: No. 6017696ember 1, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, David B.  
REGISTRATION NUMBER: 31,125  
REFERENCE/DOCKET NUMBER: 207/263  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic  
TYPE: acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-271-882B-21

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-271-882B-21 (1-19)

QY 56 HisValGluLeuLeu 60  
DB 2 CACGTAGAACTGCTC 16

RESULT 103  
US-08-855-058-2  
Sequence 2, Application US/08855058A  
Patent No. 6048690  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.  
APPLICANT: Tu, Eugene  
APPLICANT: Sosnowski, Ronald G.  
APPLICANT: O'Connell, James P.  
TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR  
TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR  
TITLE OF INVENTION: SYNTHESIS  
FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175

CURRENT APPLICATION NUMBER: US/08/855,058A  
CURRENT FILING DATE: 1997-05-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthesized  
US-08-855-058-2

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-2 (1-19)

QY 56 HisValGluLeuLeu 60  
DB 2 CACGTAGAACTGCTC 16

RESULT 104  
US-08-855-058-8  
Sequence 8, Application US/08855058A  
Patent No. 6048690  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.  
APPLICANT: Tu, Eugene  
APPLICANT: Sosnowski, Ronald G.  
APPLICANT: O'Connell, James P.  
TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR  
TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR  
FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175  
CURRENT APPLICATION NUMBER: US/08/855,058A  
CURRENT FILING DATE: 1997-05-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Human HLA  
US-08-855-058-8

Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-855-058-8 (1-19)

QY 56 HisValGluLeuLeu 60  
DB 2 CACGTAGAACTGCTC 16

RESULT 105  
US-08-855-058-9/c  
Sequence 9, Application US/08855058A  
Patent No. 6048690  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J.  
APPLICANT: Tu, Eugene  
APPLICANT: Sosnowski, Ronald G.  
APPLICANT: O'Connell, James P.

```
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-9

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-9 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAGCTGCTC 4

RESULT 106
US-08-855-058-10/c
; Sequence 10, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-10

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-10 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAGCTGCTC 4

RESULT 107
US-08-855-058-11/c
; Sequence 11, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
```

```
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-11

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-11 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 108
US-08-855-058-12/c
; Sequence 12, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-12

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-12 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 109
US-08-855-058-13/c
; Sequence 13, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
```



; APPLICANT: Sosnowski, Ronald G.  
 ; APPLICANT: O'Connell, James P.  
 ; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR  
 ; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR  
 ; TITLE OF INVENTION: SYNTHESIS  
 ; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175  
 ; CURRENT APPLICATION NUMBER: US/08/855,058A  
 ; CURRENT FILING DATE: 1997-05-14  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 13  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Human HLA  
 US-08-855-058-13

Alignment Scores:  
 Pred. No.: 1.06e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-13 (1-19)

Qy 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGAACTGCTC 4

RESULT 110  
 US-09-158-313-20  
 ; Sequence 20, Application US/09158313  
 ; Patent No. 6066725  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deboer, Herman A.  
 ; APPLICANT: Strijker, Rein  
 ; APPLICANT: Heyneker, Herbert L.  
 ; APPLICANT: Platenburg, Gerald  
 ; APPLICANT: Lee, Sang He  
 ; APPLICANT: Pieper, Frank  
 ; APPLICANT: Krimpenfort, Paul J.A.  
 ; TITLE OF INVENTION: Production of Recombinant Polypeptides  
 ; TITLE OF INVENTION: by Bovine Species and Transgenic Methods  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/158,313  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/476,798  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/895,956  
 ; FILING DATE: 15-JUN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/619,131  
 ; FILING DATE: 27-NOV-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/444,745  
 ; FILING DATE: 01-DEC-1989

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Liebescheutz, Joe O.  
 ; REGISTRATION NUMBER: 37,505  
 ; REFERENCE/DOCKET NUMBER: 16994-003125  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-543-9600  
 ; TELEFAX: 415-543-5043  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 US-09-158-313-20

Alignment Scores:  
 Pred. No.: 1.06e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-158-313-20 (1-19)

Qy 32 ValVallysArgArg 36  
 Db 5 GTTGTAACGACGG 19

RESULT 111  
 US-08-476-798-20  
 ; Sequence 20, Application US/08476798  
 ; Patent No. 6140552  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deboer, Herman A.  
 ; APPLICANT: Strijker, Rein  
 ; APPLICANT: Heyneker, Herbert L.  
 ; APPLICANT: Platenburg, Gerald  
 ; APPLICANT: Lee, Sang He  
 ; APPLICANT: Pieper, Frank  
 ; APPLICANT: Krimpenfort, Paul J.A.  
 ; TITLE OF INVENTION: Production of Recombinant Polypeptides  
 ; TITLE OF INVENTION: by Bovine Species and Transgenic Methods  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/476,798  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/077,788  
 ; FILING DATE: 15-JUN-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/895,956  
 ; FILING DATE: 15-JUN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/619,131  
 ; FILING DATE: 27-NOV-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/444,745  
 ; FILING DATE: 01-DEC-1989

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-476-798-20

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-476-798-20 (1-19)

QY 32 ValVallysArgArg 36
Db 5 GTTGTAACACGACGG 19

RESULT 112
US-08-726-278-21
; Sequence 21, Application US/08726278
; Patent No. 6238624
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Evans, Glen A.
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR
; FILE REFERENCE: DAVID B. MURPHY/NANOGEN: 222-210
; CURRENT APPLICATION NUMBER: US/08/726,278
; PRIOR FILING DATE: 1996-10-04
; PRIOR FILING DATE: 08/271,882
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for
; OTHER INFORMATION: Labeling
US-08-726-278-21

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-726-278-21 (1-19)

QY 56 HisValGluLeu 60
Db 2 CACGTAGACTGCTC 16

RESULT 113
US-09-141-286-2
```

```
; Sequence 2, Application US/09141286
; Patent No. 6245508
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; O'Connell, James P.; Juncosa,
; APPLICANT: Robert D.; Sosnowski, Ronald G.; Jackson, Thomas
; APPLICANT: R.
; TITLE OF INVENTION: METHOD FOR FINGERPRINTING UTILIZING
; TITLE OF INVENTION: AN ELECTRONICALLY ADDRESSABLE ARRAY
; TITLE OF INVENTION: (as amended)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon LLP
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,286
; FILING DATE: August 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/534,454
; FILING DATE: September 27, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 225/167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-141-286-2

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-141-286-2 (1-19)

QY 56 HisValGluLeu 60
Db 2 CACGTAGACTGCTC 16

RESULT 114
US-09-144-367-44
; Sequence 44, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
```

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; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-44

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-144-367-44 (1-19)

Qy 22 LysGlyArgArgGlu 26
Db 3 AAGGCGAGGAGAG 17

RESULT 115
US-09-536-977-100
; Sequence 100, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: BX08 CONSTRUCTS
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-977-100

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-536-977-100 (1-19)

Qy 32 ValVallyArgArg 36
Db 1 GTTCTAAACGACGG 15

RESULT 116
PCT-US93-02059-18/c
; Sequence 18, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

; ADDRESS: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
PCT-US93-02059-18

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US93-02059-18 (1-19)

Qy 179 IleLeuLeuProLeu 183
Db 17 ATTCTCTACTCTG 3

RESULT 117
5455029-5/c
; Patent No. 5455029
; APPLICANT: HARTMAN, JACOB R.; OPPENHEIM, AMOS B.; GORECKI,
; MARIAN; AVIV, HAIM; OREN, RACHEL
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING
; A MIXTURE OF HUMAN CUZIN SUPEROXIDE DISMUTASE ANALOGS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/933,500
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 449,125
; FILING DATE: 08-DEC-1989
; APPLICATION NUMBER: 202,238
; FILING DATE: 03JUN-1988
; APPLICATION NUMBER: 597,056
; FILING DATE: 14-AUG-1985
; APPLICATION NUMBER: 767,143
; FILING DATE: 19-AUG-1985
; APPLICATION NUMBER: 544,245
; FILING DATE: 27-AUG-1984
; SEQ ID NO: 5
; LENGTH: 19
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5455029-5  
Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x 5455029-5 (1-19)  
QY 69 AspleuAspProgly 73  
DB 18 GATCTAGACCGGGA 4  
RESULT 118  
5455029-25/c  
;PATENT NO. 5455029  
; APPLICANT: HARTMAN, JACOB R.; OPPENHEIM, AMOS B.; GORECKI,  
; MARIAN; AVIV, HAIM; OREN, RACHEL  
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING  
; A MIXTURE OF HUMAN CUZIN SUPEROXIDE DISMUTASE ANALOGS  
; NUMBER OF SEQUENCES: 30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/933,500  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 449,125  
; FILING DATE: 08-DEC-1989  
; APPLICATION NUMBER: 202,238  
; FILING DATE: 03JUN-1988  
; APPLICATION NUMBER: 897,056  
; FILING DATE: 14-AUG-1985  
; APPLICATION NUMBER: 767,143  
; FILING DATE: 19-AUG-1985  
; APPLICATION NUMBER: 644,245  
; FILING DATE: 27-AUG-1984  
; SEQ ID NO: 25:  
; LENGTH: 19  
5455029-25  
Alignment Scores:  
Pred. No.: 1.06e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x 5455029-25 (1-19)  
QY 69 AspleuAspProgly 73  
DB 18 GATCTAGACCGGGA 4  
RESULT 119  
US-07-664-989B-104/c  
; Sequence 104, Application US/07664989B  
; Patent No. 5223409  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; APPLICANT: Guterman, Sonia Kosow  
; APPLICANT: Roberts, Bruce Lindsay  
; APPLICANT: Markland, William  
; APPLICANT: Lev, Arthur Charles  
; APPLICANT: Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.

STREET: Suite 300  
CITY: Washington,  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 4.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/664,989B  
FILING DATE: 19910301  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US89/03731  
FILING DATE: 01-SEP-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/487,063  
FILING DATE: 02-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/240,160  
FILING DATE: 02-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Iver P.  
REGISTRATION NUMBER: 28005  
REFERENCE/DOCKET NUMBER: LADNER 7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: genomic DNA  
US-07-664-989B-104  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-07-664-989B-104 (1-20)  
QY 178 ArgileLeuLeuPro 182  
DB 18 CGGATCCTCCTCCT 4  
RESULT 120  
US-07-931-473B-59  
; Sequence 59, Application US/07931473B  
; Patent No. 5270163  
; GENERAL INFORMATION:  
; APPLICANT: Larry Gold  
; APPLICANT: Craig Tuerk  
; TITLE OF INVENTION: Nucleic Acid Ligands  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Beaton & Swanson, P.C.  
; STREET: 4582 South Ulster Street Parkway, #403  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80237  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS

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; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/931.473B
; FILING DATE: 19920817
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-931-473B-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-931-473B-59 (1-20)
QY 32 ValVallysArgArg 36
Db 4 GTTGTAACGACGG 18

RESULT 121
US-07-714-131C-59
; Sequence 59, Application US/07714131C
; Patent No. 5475096
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714.131C
; FILING DATE: June 10, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-714-131C-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-714-131C-59 (1-20)
QY 32 ValVallysArgArg 36
Db 4 GTTGTAACGACGG 18

RESULT 122
US-07-872-678A-13/c
; Sequence 13, Application US/07872678A
; Patent No. 5541060
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme, et al.
; TITLE OF INVENTION: DETECTION OF EARLY-ONSET
; TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: Post Office Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,678A
; FILING DATE: 22-APRIL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: ARCD016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA ( genomic)
US-07-872-678A-13

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-872-678A-13 (1-20)
QY 104 LeuSerLeuArgIle 108
Db 18 TTGAGCCTCAGATC 4

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RESULT 123
US-08-271-946A-20
; Sequence 20, Application US/08271946A
; Patent No. 5545527
; GENERAL INFORMATION:
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.946A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 21 of human RBL gene
; US-08-271-946A-20
Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-271-946A-20 (1-20)
QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16
RESULT 124
US-08-271-942A-20
; Sequence 20, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
```

```
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 21 of human RBL gene
; US-08-271-942A-20
Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-271-942A-20 (1-20)
QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16
RESULT 125
US-08-259-745A-47
; Sequence 47, Application US/08259745A
; Patent No. 5582983
; GENERAL INFORMATION:
; APPLICANT: Anderson, Donald
; APPLICANT: Scholin, Christopher
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS OF IDENTIFYING ALEXANDRIUM
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
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; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,745A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/967,637
; FILING DATE: 28-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Neuner, George W.
; REGISTRATION NUMBER: 26,964
; REFERENCE/DOCKET NUMBER: 42,101 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-259-745A-47

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-259-745A-47 (1-20)

QY 170 ValArgLeuSerArg 174
Db 6 GTCCGTCCTTCAAGA 20

RESULT 126
US-08-146-504-7/c
; Sequence 7, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible

```

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; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,504
; FILING DATE: No. 5605662ember 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-146-504-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-146-504-7 (1-20)

QY 56 HisValGluLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 127
US-08-306-546C-3
; Sequence 3, Application US/08306546C
; Patent No. 5605797
; GENERAL INFORMATION:
; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,546C
; FILING DATE: September 15, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003

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none

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Primer
US-08-306-546C-3

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-306-546C-3 (1-20)
QY 179 IleLeuLeuProLeu 183
Db 6 ATTCTTTACCCCTG 20

RESULT 128
US-08-170-689-1
; Sequence 1, Application US/08170689
; Patent No. 5624798
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NOBUKO
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: TOMIDA, YOSHINORI
; APPLICANT: MIYAZAKI, TAKESHI
; APPLICANT: KAWAGUCHI, YASUHIRO
; TITLE OF INVENTION: FLUORESCENT STAIN CONTAINING
; TITLE OF INVENTION: OF PYLIUM SALT OR ITS SIMILAR SALT, DETECTION METHOD
; TITLE OF INVENTION: OF NUCLEIC ACID BY USE OF IT, AND FLUORESCENT
; TITLE OF INVENTION: STAINING METHOD OF BIOLOGICAL SAMPLE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 277 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: UNITED STATES
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,689
; FILING DATE: 21-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WOLLMAN, PENINA
; REGISTRATION NUMBER: 30,816
; REFERENCE/DOCKET NUMBER: 35.C9616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-212-758-2400
; TELEFAX: 1-212-758-2382
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-170-689-1

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Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-170-689-1 (1-20)
QY 32 ValVallysArg 36
Db 1 GTTGTAACGACGG 15

RESULT 129
US-08-412-110-59
; Sequence 59, Application US/08412110
; Patent No. 5670637
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESS: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,110
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-412-110-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-412-110-59 (1-20)
QY 32 ValVallysArg 36
Db 4 GTTGTAACGACGG 18

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RESULT 130  
US-08-317-872A-1  
; Sequence 1, Application US/08317872A  
; Patent No. 5679516  
; GENERAL INFORMATION:  
; APPLICANT: OKAMOTO, TADASHI  
; APPLICANT: MIYAZAKI, TAKESHI  
; TITLE OF INVENTION: PROCESS FOR DETECTING NUCLEIC ACID  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO  
; STREET: 277 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: UNITED STATES  
; ZIP: 10172-0174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/317,872A  
; FILING DATE: 04-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXON, PETER  
; REGISTRATION NUMBER: 24,947  
; REFERENCE/DOCKET NUMBER: 35C10188  
; TELEPHONE: 1-212-758-2400  
; TELEFAX: 1-212-758-2982  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (SYNTHESIZED POLYNUCLEOTIDE)  
US-08-317-872A-1  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-317-872A-1 (1-20)  
Qy 32 ValVallysargArg 36  
Db 1 GTTGTAACGACGG 15  
RESULT 131  
US-08-317-872A-2/c  
; Sequence 2, Application US/08317872A  
; Patent No. 5679516  
; GENERAL INFORMATION:  
; APPLICANT: OKAMOTO, TADASHI  
; APPLICANT: MIYAZAKI, TAKESHI  
; TITLE OF INVENTION: PROCESS FOR DETECTING NUCLEIC ACID  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO  
; STREET: 277 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: UNITED STATES  
; ZIP: 10172-0174  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,872A  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXON, PETER  
REGISTRATION NUMBER: 24,947  
REFERENCE/DOCKET NUMBER: 35C10188  
TELEPHONE: 1-212-758-2400  
TELEFAX: 1-212-758-2982  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (SYNTHESIZED POLYNUCLEOTIDE)  
US-08-317-872A-2  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-317-872A-2 (1-20)  
Qy 32 ValVallysargArg 36  
Db 20 GTTGTAACGACGG 6  
RESULT 132  
US-08-255-892-36  
; Sequence 36, Application US/08255892  
; Patent No. 5695926  
; GENERAL INFORMATION:  
; APPLICANT: CROS, PHILIPPE  
; APPLICANT: ALLIBERT, PATRICE  
; APPLICANT: MALLEET, FRANCOIS  
; APPLICANT: MABILAT, CLAUDE  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION  
; TITLE OF INVENTION: TECHNIQUE  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/255,892  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/834,543  
; FILING DATE: 11-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DEEVER, DONALD B.

REGISTRATION NUMBER: 23,048  
REFERENCE/DOCKET NUMBER: 1032/94109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-966-880A-8 (1-198) x US-08-409-442A-59 (1-20)

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-255-892-36 (1-20)

Qy 174 ArginLeuArgArg 178  
Db 1 AGACAGCTCAGAAGA 15

## RESULT 133

US-08-409-442A-59  
Sequence 59, Application US/08409442A  
Patent No. 5696249  
GENERAL INFORMATION:

APPLICANT: Larry Gold  
APPLICANT: Craig Tuerk  
TITLE OF INVENTION: Nucleic Acid Ligands  
NUMBER OF SEQUENCES: 374  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,442A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: June 10, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: June 11, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX01/C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-409-442A-59

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-409-442A-59 (1-20)

Qy 32 ValVallysArgArg 36  
Db 4 GTTGTAAACGACGG 18

## RESULT 134

US-08-671-829-1  
Sequence 1, Application US/08671829  
Patent No. 5705346  
GENERAL INFORMATION:

APPLICANT: OKAMOTO, TADASHI  
APPLICANT: TOMIDA, YOSHINORI  
APPLICANT: YAMAMOTO, NOBUKO  
APPLICANT: KAWAGUCHI, MASAHIRO  
APPLICANT: MAKINO, KEISUKE  
APPLICANT: MURAKAMI, AKIRA  
TITLE OF INVENTION: METHOD FOR DETECTING TARGET  
TITLE OF INVENTION: NUCLEIC ACID  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto  
STREET: 277 Park Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,829  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/157,427  
FILING DATE: 26-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Wollman, Penina  
REGISTRATION NUMBER: 30,816  
REFERENCE/DOCKET NUMBER: 35.C9569  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-2400  
TELEFAX: 212-758-2982  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-671-829-1

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-671-829-1 (1-20)

QY 32 ValValValArgArg 36  
 Db 1 GTTGTAAACGACGG 15

RESULT 135  
 US-08-555-678-49/c  
 ; Sequence 49, Application US/08555678  
 ; Patent No. 5763174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nishikura, Kazuko  
 ; TITLE OF INVENTION: RNA Editing Enzyme and Methods  
 ; TITLE OF INVENTION: of Use Thereof  
 ; NUMBER OF SEQUENCES: 67  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howson and Howson  
 ; STREET: Spring House Corporate Cntr, P.O. Box 457  
 ; CITY: Spring House  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19477  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/555,678  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/197,794  
 ; FILING DATE: 17-FEB-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/280,443  
 ; FILING DATE: 25-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/457,459  
 ; FILING DATE: 01-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bak, Mary E.  
 ; REGISTRATION NUMBER: 31,215  
 ; REFERENCE/DOCKET NUMBER: WST49DUSA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-540-9206  
 ; TELEFAX: 215-540-5818  
 ; INFORMATION FOR SEQ ID NO: 49:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "primer"  
 US-08-555-678-49

Alignment Scores:  
 Pred. No.: 1.11e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 Db: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-555-678-49 (1-20)

QY 38 SerAlaThrSerPhe 42  
 Db 17 TCAGCCACATCCTC 3

RESULT 136  
 US-08-753-147-100  
 ; Sequence 100, Application US/08753147

Patent No. 5770372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Concannon, Patrick  
 ; TITLE OF INVENTION: Detection of Mutations in the Human ATM Gene  
 ; NUMBER OF SEQUENCES: 196  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Christensen O'Connor Johnson and Kindness  
 ; STREET: 1420 5th Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98101-2347  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/753,147  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sheiness, Diana K.  
 ; REGISTRATION NUMBER: 35,356  
 ; REFERENCE/DOCKET NUMBER: VMRC-1-9714  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 743-4387  
 ; TELEFAX: (206) 224 0779  
 ; INFORMATION FOR SEQ ID NO: 100:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 US-08-753-147-100

Alignment Scores:  
 Pred. No.: 1.11e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 Db: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-753-147-100 (1-20)

QY 97 PheLeuArgGlyAsn 101  
 Db 4 TTTCTTAGAGGAAT 18

RESULT 137  
 US-08-464-531-44/c  
 ; Sequence 44, Application US/08464531  
 ; Patent No. 5789184  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: BROACH, Jim  
 ; APPLICANT: MANFREDI, John  
 ; APPLICANT: KLEIN, Christine  
 ; APPLICANT: MURPHY, Andrew J.  
 ; APPLICANT: PAUL, Jeremy  
 ; APPLICANT: TRUEHEART, Joshua  
 ; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
 ; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
 ; NUMBER OF SEQUENCES: 119  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,531  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/322,137  
 FILING DATE: 13-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/309,313  
 FILING DATE: 20-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/190,328  
 FILING DATE: 31-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/041,431  
 FILING DATE: 31-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COOPER, Iver P.  
 REGISTRATION NUMBER: 28,005  
 REFERENCE/DOCKET NUMBER: FOLWKS=2G  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-464-531-44

Alignment Scores:  
 Pred. No.: 1,11e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-464-531-44 (1-20)

QY 104 LeuSerLeuArgile 108  
 Db 18 CTGAGTCCTCGCATC 4

RESULT 138  
 US-08-530-524A-3  
 Sequence 3, Application US/08530524A  
 Patent No. 5837836  
 GENERAL INFORMATION:  
 APPLICANT: Friderici, Karen  
 APPLICANT: Jones, Margaret  
 APPLICANT: Chen, Hong  
 APPLICANT: Cavanagh, Kevin  
 TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods  
 TITLE OF INVENTION: of Use  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 STREET: P.O. Box 828  
 CITY: Bloomfield Hills  
 STATE: Michigan

COUNTRY: USA  
 ZIP: 48303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/530,524A  
 FILING DATE: September 19, 1995  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, Deann F.  
 REGISTRATION NUMBER: 36,683  
 REFERENCE/DOCKET NUMBER: 6550-00003DVA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (810)641-1600  
 TELEFAX: (810)641-0270  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: primer  
 US-08-530-524A-3

Alignment Scores:  
 Pred. No.: 1,11e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-530-524A-3 (1-20)

QY 179 IleLeuLeuProtein 183  
 Db 6 ATTCTTTTACCCCTG 20

RESULT 139  
 US-08-467-007A-2  
 Sequence 2, Application US/08467007A  
 Patent No. 5840875  
 GENERAL INFORMATION:  
 APPLICANT: Schreiner, George F.  
 APPLICANT: Meyer, Timothy W.  
 APPLICANT: Oberbauer, Rainer  
 TITLE OF INVENTION: Method For Administering Antisense  
 TITLE OF INVENTION: Oligonucleotides  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Banner & Allegretti, Ltd.  
 STREET: 10 South Wacker, Suite 3000  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: hard disc  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,007A  
 FILING DATE: 06/06/95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Blair Hughes  
 REGISTRATION NUMBER: 32,901  
 REFERENCE/DOCKET NUMBER: 95,728  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-467-007A-2  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-467-007A-2 (1-20)  
QY 102 ProAsnLeuSerLeu 106  
Db 5 CCCATCTCTCGTG 19  
RESULT 140  
US-08-469-609A-59  
; Sequence 59, Application US/08469609A  
; Patent No. 5843653  
; GENERAL INFORMATION:  
; APPLICANT: Larry Gold  
; APPLICANT: Craig Tuerk  
; TITLE OF INVENTION: Nucleic Acid Ligands  
; NUMBER OF SEQUENCES: 374  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,609A  
; FILING DATE: June 6, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,964  
; FILING DATE: April 25, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/412,110  
; FILING DATE: March 27, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/409,442  
; FILING DATE: March 24, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: June 10, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: June 11, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX01/C5  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 nucleotides

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-469-609A-59  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-469-609A-59 (1-20)  
QY 32 ValVallysArgArg 36  
Db 4 GTTGTAAACGACGG 18  
RESULT 141  
US-08-117-952-475/c  
; Sequence 475, Application US/08117952  
; Patent No. 5851760  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; APPLICANT: Smith, Michael W.  
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
; NUMBER OF SEQUENCES: 797  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,952  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/078,471  
; FILING DATE: 15-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9423  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Oligonucleotide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-117-952-475  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-117-952-475 (1-20)
QY 127 ArgArgLeuHisArg 131
Db 18 AGAAGACTGCACAGA 4

RESULT 142
US-08-117-952-646/c
; Sequence 646, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 646:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-117-952-646

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-117-952-646 (1-20)
QY 57 ValGluLeuPhe 61
Db 18 GTTGAGCTGCTTC 4

RESULT 143
US-08-461-598-44/c
; Sequence 44, Application US/08461598
; Patent No. 5876951
; GENERAL INFORMATION:

```

```

; APPLICANT: FOLWES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,598
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWES-2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-461-598-44

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-461-598-44 (1-20)
QY 104 LeuSerLeuArgile 108
Db 18 CTGAGTCTTCGATC 4

RESULT 144
US-08-832-658A-5
; Sequence 5, Application US/08832658A
; Patent No. 5914269

```

```

; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF EPIDERMAL
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5914269ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,658A
; FILING DATE: April 4, 1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-832-658A-5

```

```

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-832-658A-5 (1-20)

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Qy 129 LeuHisArgAlagly 133
Db 6 TTGCACAGGGCAGGG 20

```

RESULT 145

```

; US-08-725-976-7/c
; Sequence 7, Application US/08725976
; Patent No. 5929208
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: WINDOWS (VERSION 3.0)
; SOFTWARE: WordPerfect (Version 6.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,976
; FILING DATE: October 4, 1996

```

```

; CLASSIFICATION: 422
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 5929208ember 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murthy, David B
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 222/211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-725-976-7

```

```

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

```

US-09-966-880A-8 (1-198) x US-08-725-976-7 (1-20)

```

Qy 56 HisValgluLeuLeu 60
Db 18 CACGTAGACTGCTC 4

```

RESULT 146

```

; US-08-683-918-1
; Sequence 1, Application US/08683918
; Patent No. 5939256
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NUBUKO
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: TOMIDA, YOSHINORI
; APPLICANT: KAWAGUCHI, MASAHITO
; APPLICANT: MAKINO, KEISUKE
; APPLICANT: MURAKAMI, AKIRA
; TITLE OF INVENTION: METHOD FOR DETECTION OF NUCLEIC
; TITLE OF INVENTION: ACID AND PROBE THEREFOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 277 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,918
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/157,318
; FILING DATE: 26-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WOLLMAN, PENINA
; REGISTRATION NUMBER: 30,816
; REFERENCE/DOCKET NUMBER: 35.C9568

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-2400
; TELEFAX: 212-758-2982
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-683-918-1
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-683-918-1 (1-20)
QY 32 ValVallyArqArq 36
Db 1 GTGTAAACGACGG 15

RESULT 147
US-09-166-203-45
; Sequence 45, Application US/09166203A
; Patent No. 5988826
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowert, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; FILE REFERENCE: ISPH-0323
; CURRENT APPLICATION NUMBER: US/09/166,203A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-203-45
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-166-203-45 (1-20)
QY 181 LeuProLeuTy-Glu 185
Db 1 TTGCCCTTATATGAG 15

RESULT 148
US-08-888-982A-4
; Sequence 4, Application US/08888982A
; Patent No. 5981731
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 East Main Street

```

```

; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,982A
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 5981731ember 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-888-982A-4
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-888-982A-4 (1-20)
QY 169 SerValArgLeuSer 173
Db 4 TCTGTAAAGCCTTCA 18

RESULT 149
US-08-271-882B-7/c
; Sequence 7, Application US/08271882B
; Patent No. 6017696
; GENERAL INFORMATION:
; APPLICANT: Michael J. Heller
; APPLICANT: Eugene Tu
; APPLICANT: Glen A. Evans
; APPLICANT: Ronald G. Soenowski
; TITLE OF INVENTION: SELF-ADDRESSABLE
; TITLE OF INVENTION: SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND
; TITLE OF INVENTION: DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS
; TITLE OF INVENTION: AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California

```



```

; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,882B
; FILING DATE: July 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 6017696member 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 207/263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-882B-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-271-882B-7 (1-20)

QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 150
US-08-782-798-1
; Sequence 1, Application US/08782798
; Patent No. 6022961
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NOBUKO
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: TOMIDA, YOSHINORI
; APPLICANT: MIYAZAKI, TAKESHI
; APPLICANT: KAWAGUCHI, MASASHIRO
; TITLE OF INVENTION: FLUORESCENT STAIN CONTAINING
; TITLE OF INVENTION: PYRYLIUM SALT OR ITS SIMILAR SALT, DETECTION METHOD
; TITLE OF INVENTION: OF NUCLEIC ACID BY USE OF IT, AND FLUORESCENT
; TITLE OF INVENTION: STAINING METHOD OF BIOLOGICAL SAMPLE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 277 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: UNITED STATES
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,798
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/170,689
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WOLLMAN, PENINA
; REGISTRATION NUMBER: 30,816
; REFERENCE/DOCKET NUMBER: 35.C9616 DIV.I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-212-758-2400
; TELEFAX: 1-212-758-2982
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
; US-08-782-798-1

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-782-798-1 (1-20)

QY 32 ValVallylsArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 151
US-08-779-916A-20
; Sequence 20, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 21 of human RBL gene
US-08-779-916A-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-779-916A-20 (1-20)

QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTATGTT 16

RESULT 152
US-08-777-266A-69
; Sequence 69, Application US/08777266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20

```

```

; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-777-266A-69

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-777-266A-69 (1-20)

QY 176 LeuAtcAtcGileu 180
DB 1 CTGCGCGGAATCCTG 15

RESULT 153
US-08-322-137-44/c
; Sequence 44, Application US/08322137
; Patent No. 6100042
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHORMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,137
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-322-137-44

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-322-137-44 (1-20)
QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 154
US-09-143-190-59
; Sequence 59, Application US/09143190
; Patent No. 6110900
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Turk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,190
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

US-09-143-190-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-143-190-59 (1-20)
QY 32 valvallyeArgArg 36
Db 4 GTTGTAAACGACGG 18

RESULT 155
US-08-600-982-20/c
; Sequence 20, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,982
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: PCR primer; see TABLE 1
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-600-982-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-600-982-20 (1-20)
QY 59 LeuLeuPheLeuArg 63

```

DB 19 TTGCTATTCTCAGA 5  
RESULT 156  
US-09-418-641-39  
; Sequence 39, Application US/09418641A  
; Patent No. 6124133  
; GENERAL INFORMATION:  
; APPLICANT: Jennifer K. Taylor  
; APPLICANT: Lex M. Coweert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION  
; FILE REFERENCE: RTS-0105  
; CURRENT APPLICATION NUMBER: US/09/418.641A  
; CURRENT FILING DATE: 1999-10-15  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 39  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-418-641-39  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 3  
US-09-966-880A-8 (1-198) x US-09-418-641-39 (1-20)  
QY 59 LeuLeuPheLeuArg 63  
DB 6 CTCCTCTTCCTCCGG 20  
RESULT 157  
US-09-069-886-34  
; Sequence 34, Application US/09069886  
; Patent No. 6132724  
; GENERAL INFORMATION:  
; APPLICANT: Blum, Kenneth  
; APPLICANT: Comings, David E.  
; APPLICANT: Ivy, John L.  
; TITLE OF INVENTION: ALLELIC POLYGENE DIAGNOSIS OF REWARD  
; TITLE OF INVENTION: DEFICIENCY SYNDROME AND TREATMENT  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,886  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: BLUM:002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512)418-3000  
; TELEFAX: (512)474-7577  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-069-886-34  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 3  
US-09-966-880A-8 (1-198) x US-09-069-886-34 (1-20)  
QY 22 LysGlyArgAcGlu 26  
DB 5 AAGGGAAGGAGGAA 19  
RESULT 158  
US-09-428-584-14  
; Sequence 14, Application US/09428584  
; Patent No. 6136604  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF METHIONINE AMINOPEPTIDASE 2 EXPRESSION  
; FILE REFERENCE: RTS-0114  
; CURRENT APPLICATION NUMBER: US/09/428,584  
; CURRENT FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-428-584-14  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0  
DB: 3  
US-09-966-880A-8 (1-198) x US-09-428-584-14 (1-20)  
QY 70 LeuAspProGlyArg 74  
DB 6 CTGGATCCAGGTGCG 20  
RESULT 159  
US-08-882-046-31/c  
; Sequence 31, Application US/08882046  
; Patent No. 6136952  
; GENERAL INFORMATION:  
; APPLICANT: Li, Linheng  
; APPLICANT: Hood, Leroy  
; APPLICANT: Krantz, Ian D.  
; APPLICANT: Spinner, Nancy B.  
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding  
; TITLE OF INVENTION: Nucleic Acids and Methods of Use  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,046  
FILING DATE: 25-JUN-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UW 2637  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1..10  
FEATURE:  
NAME/KEY: intron  
LOCATION: 11..20  
US-08-882-046-31  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-882-046-31 (1-20)  
QY 27 ThrTyrLeuCysTyr 31  
Db 16 ACATACCTCTGTAC 2  
RESULT 160  
US-09-444-053-19/c  
Sequence 19, Application US/09444053A  
Patent No. 6165728  
GENERAL INFORMATION:  
APPLICANT: Donna T. Ward  
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION  
FILE REFERENCE: RTS-0122  
CURRENT APPLICATION NUMBER: US/09/444,053A  
CURRENT FILING DATE: 1999-11-19  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 19  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-444-053-19  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-444-053-19 (1-20)

QY 163 GluGlyLeuHisGlu 167  
Db 15 GAAGGACTCCATGAA 1  
RESULT 161  
US-09-444-053-20/c  
Sequence 20, Application US/09444053A  
Patent No. 6165728  
GENERAL INFORMATION:  
APPLICANT: Donna T. Ward  
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION  
FILE REFERENCE: RTS-0122  
CURRENT APPLICATION NUMBER: US/09/444,053A  
CURRENT FILING DATE: 1999-11-19  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 20  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-444-053-20  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-444-053-20 (1-20)  
QY 163 GluGlyLeuHisGlu 167  
Db 20 GAAGGACTCCATGAA 6  
RESULT 162  
US-09-433-694-63  
Sequence 63, Application US/09433694  
Patent No. 6165790  
GENERAL INFORMATION:  
APPLICANT: Alexander H. Borchers  
APPLICANT: Donna T. Ward  
TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P55 GAMMA EXPRESSION  
FILE REFERENCE: RTS-0098  
CURRENT APPLICATION NUMBER: US/09/433,694  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 63  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-433-694-63  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-433-694-63 (1-20)  
QY 29 LeuCysTyrValVal 33  
Db 3 CTTTGTATGTTGTT 17

RESULT 163  
US-09-435-296-73  
; Sequence 73, Application US/09435296  
; Patent No. 6171860  
; GENERAL INFORMATION:  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Lex M. Cowert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RANK EXPRESSION  
; FILE REFERENCE: RTS-0116  
; CURRENT APPLICATION NUMBER: US/09/435,296  
; CURRENT FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-435-296-73  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-435-296-73 (1-20)  
QY 128 ArgLeuHisArgAla 132  
|||||  
DB 2 AGGCTGCACCGGCT 16  
RESULT 164  
US-09-306-876A-7  
; Sequence 7, Application US/09306876A  
; Patent No. 6187585  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Lipton, Allan  
; APPLICANT: Witters, Lois M  
; TITLE OF INVENTION: Oligonucleotide Inhibition of Epidermal Growth Factor  
; FILE REFERENCE: ISIS3509  
; CURRENT APPLICATION NUMBER: US/09/306,876A  
; CURRENT FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 08/832,658  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6187585el  
US-09-306-876A-7  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-306-876A-7 (1-20)  
QY 129 LeuHisArgAlaGly 133  
|||||

DB 6 TTGCACAGGCGCAGG 20  
RESULT 165  
US-09-234-434-2/c  
; Sequence 2, Application US/09234434  
; Patent No. 6197532  
; GENERAL INFORMATION:  
; APPLICANT: Rao, Prakash N. et al.  
; TITLE OF INVENTION: Diagnosis and Detection of Breast Cancer and Other  
; FILE REFERENCE: Rao 9706M.1  
; CURRENT APPLICATION NUMBER: US/09/234,434  
; CURRENT FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 60/122,048  
; PRIOR FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCT primer  
US-09-234-434-2  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x US-09-234-434-2 (1-20)  
QY 179 IleLeuLeuProLeu 183  
|||||  
DB 19 ATCCTCTGCCTCTG 5  
RESULT 166  
US-09-446-504-67  
; Sequence 67, Application US/09446504  
; Patent No. 6218150  
; GENERAL INFORMATION:  
; APPLICANT: UEMORI, Takashi  
; APPLICANT: SATO, Yoshimi  
; APPLICANT: FUJITA, Tomoko  
; APPLICANT: MIYAKE, Kazuo  
; APPLICANT: MUKAI, Hiroyuki  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS  
; FILE REFERENCE: 1422-408PCT  
; CURRENT APPLICATION NUMBER: US/09/446,504  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: PCT/JP98/02845  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: JP 9-187496  
; PRIOR FILING DATE: 1997-06-26  
; PRIOR APPLICATION NUMBER: JP 9-320692  
; PRIOR FILING DATE: 1997-11-27  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-446-504-67  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-446-504-67 (1-20)

QY 156 GluArgThrPheLeu 160  
DB 3 GAGAGAACTTCAAG 17

RESULT 167

US-08-726-278-7/c  
; Sequence 7, Application US/08726278  
; Patent No. 6238624  
; GENERAL INFORMATION:  
; APPLICANT: Heller, Michael J.  
; APPLICANT: Tu, Eugene  
; APPLICANT: Evans, Glen A.  
; APPLICANT: Sosnowski, Ronald G.  
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR  
; FILE REFERENCE: BIOLOGICAL ANALYSIS AND DIAGNOSTICS  
; CURRENT APPLICATION NUMBER: 222-210  
; CURRENT FILING DATE: 1996-10-04  
; PRIOR APPLICATION NUMBER: 08/271,882  
; PRIOR FILING DATE: 1994-07-07  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for  
; OTHER INFORMATION: Labeling  
US-08-726-278-7

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-726-278-7 (1-20)

QY 56 HisValGluLeu 60  
DB 18 CACGTAGACTGCTC 4

RESULT 168

US-09-180-437-239  
; Sequence 239, Application US/09180437  
; Patent No. 6251873  
; GENERAL INFORMATION:  
; APPLICANT: FUKUSAKO, Shioji  
; APPLICANT: MORISAWA, Yoshifumi  
; APPLICANT: KUSUYAMA, Takeshi  
; TITLE OF INVENTION: Antisense Compounds to CD14  
; FILE REFERENCE: 1110-209P  
; CURRENT APPLICATION NUMBER: US/09/180,437  
; CURRENT FILING DATE: 1998-11-06  
; EARLIER APPLICATION NUMBER: PCT/JP98/00953  
; EARLIER FILING DATE: 1998-03-09  
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN  
; EARLIER FILING DATE: 1997-03-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 239  
; LENGTH: 20

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic  
; OTHER INFORMATION: acid  
US-09-180-437-239

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-180-437-239 (1-20)

QY 169 SerValArgLeuSer 173  
DB 4 AGTGCAGGTATCC 18

RESULT 169

US-08-582-333A-47/c  
; Sequence 47, Application US/08582333A  
; Patent No. 6255059  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; APPLICANT: Murphy, Andrew J. M.  
; TITLE OF INVENTION: Methods and Compositions for  
; TITLE OF INVENTION: Identifying Receptor Effectors  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,333A  
; FILING DATE: 17-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Catherine J. Kara  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: CPI-012CPS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-4214  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-582-333A-47

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-582-333A-47 (1-20)

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; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-875-243-4
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-875-243-4 (1-20)
QY 32 ValVallysargarg 36
Db 5 GTTGTAAACGACGG 19
RESULT 172
US-09-377-309-45
; Sequence 45, Application US/09377309B
; Patent No. 6258790
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowert, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; FILE REFERENCE: ISPH-0390
; CURRENT APPLICATION NUMBER: US/09/377,309B
; CURRENT FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 09/166,203
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-309-45
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-377-309-45 (1-20)
QY 181 LeuProLeuTyrglu 185
Db 1 TTGCCCTTATGAG 15
RESULT 173
US-09-377-309-71
; Sequence 71, Application US/09377309B
; Patent No. 6258790
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowert, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; FILE REFERENCE: ISPH-0390

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; CURRENT APPLICATION NUMBER: US/09/377,309B  
; CURRENT FILING DATE: 1999-08-19  
; EARLIER APPLICATION NUMBER: 09/166,203  
; EARLIER FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 99  
; SEQ ID NO 71  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-377-309-71  
  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-09-377-309-71 (1-20)  
  
QY 181 LeuProLeuTyrGlu 185  
DB 4 TTGCCCTTATGAG 18  
  
RESULT 174  
US-09-489-869-34/c  
; Sequence 34, Application US/09489869A  
; Patent No. 6268151  
; GENERAL INFORMATION:  
; APPLICANT: Susan Murray  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE MIGRATION INHIBITORY FACTOR  
; FILE REFERENCE: RTS-0110  
; CURRENT APPLICATION NUMBER: US/09/489,869A  
; CURRENT FILING DATE: 2000-01-20  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 34  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-489-869-34  
  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-09-489-869-34 (1-20)  
  
QY 125 GlyLeuArgArgLeu 129  
DB 17 GGCCTTCGCGGCTC 3  
  
RESULT 175  
US-08-750-232-20  
; Sequence 20, Application US/08750232  
; Patent No. 6270963  
; GENERAL INFORMATION:  
; APPLICANT: Visible Genetics Inc.  
; APPLICANT: Stevens, John K.  
; APPLICANT: Dunn, James M.  
; APPLICANT: Capatos, Denis  
; APPLICANT: Matthews, David E.  
; TITLE OF INVENTION: Method for Testing for Mutations in DNA

; TITLE OF INVENTION: from a Patient Sample  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: 1992 Commerce Street, Suite 309  
; CITY: Yorktown Heights  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10598-4412  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750,232  
; FILING DATE: 08-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/271,946  
; FILING DATE: 08-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 245-3252  
; TELEFAX: (914) 962-4330  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: primer for exon 21 of human RB1 gene  
US-08-750-232-20  
  
Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-08-750-232-20 (1-20)  
  
QY 28 TyrLeuCytyrVal 32  
DB 2 TACCTATGTATGTT 16  
  
RESULT 176  
US-09-428-583-34  
; Sequence 34, Application US/09428583  
; Patent No. 6271029  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSOLIN-2 EXPRESSION  
; FILE REFERENCE: RTS-0096  
; CURRENT APPLICATION NUMBER: US/09/428,583  
; CURRENT FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 34  
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-34

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-428-583-34 (1-20)
QY 56 HisValGluLeu 60
Db 6 CATGTTGAACCTCTT 20

RESULT 177
; Sequence 64, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOHESIN-2 EXPRESSION
; FILE REFERENCE: RTS-0096
; CURRENT APPLICATION NUMBER: US/09/428,583
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-64

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-428-583-64 (1-20)
QY 194 ArgThrLeuGlyLeu 198
Db 3 CGGACATTGGGATTG 17

RESULT 178
; Sequence 182, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```
US-09-593-711A-182

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-593-711A-182 (1-20)
QY 172 LeuSerArgGlnLeu 176
Db 3 CTCGCGGACAGCTG 17

RESULT 179
; Sequence 12, Application US/08682767
; Patent No. 6291741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,767
; FILING DATE: 30-July-96
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 51735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
US-08-682-767-12

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-12 (1-20)
QY 32 ValVallyArgArg 36
Db 2 GTGTAAACGACGG 16

RESULT 180
; Sequence 16, Application US/08682767
; Feature:
```

```
/ Patent No. 6291741
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ STREET: 1185 Avenue of The Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/682,767
/ FILING DATE: 30-July-96
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 51735
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0526
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
/ US-08-682-767-15

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-16 (1-20)
QY 32 ValVallyeArg 36
Db 2 GTGTAAACGACGG 16

RESULT 181
US-08-682-767-18
/ Sequence 18, Application US/08682767
/ Patent No. 6291741
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ STREET: 1185 Avenue of The Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/682,767
```

```
/ FILING DATE: 30-July-96
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 51735
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0526
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
/ US-08-682-767-18

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-18 (1-20)
QY 32 ValVallyeArg 36
Db 2 GTGTAAACGACGG 16

RESULT 182
US-09-484-617-147/c
/ Sequence 147, Application US/09484617
/ Patent No. 6303374
/ GENERAL INFORMATION:
/ APPLICANT: Hong Zhang
/ TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
/ FILE REFERENCE: RIS-0103
/ CURRENT APPLICATION NUMBER: US/09/484,617
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 176
/ SEQ ID NO 147
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
/ US-09-484-617-147

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-484-617-147 (1-20)
QY 41 SerPheSerleuAsp 45
Db 15 TCCTTCTCCCTGGAC 1

RESULT 183
US-09-721-822A-43
/ Sequence 43, Application US/09721822A
/ Patent No. 6306606
/ GENERAL INFORMATION:
/ APPLICANT: Michael J. Weber
/ OTHER INFORMATION: Antisense Oligonucleotide
```

```
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF MP-1 EXPRESSION
; FILE REFERENCE: RTS-0142
; CURRENT APPLICATION NUMBER: US/09/721,822A
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-721-822A-43

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:              4           Gaps:         0

US-09-966-880A-8 (1-198) x US-09-721-822A-43 (1-20)

QY      72 ProGlyArgCysTyr 76
Db      2 CCTGCTAGGTGTTAT 16

RESULT 184
US-09-326-186B-69
; Sequence 69, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPR-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-326-186B-69

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:              4           Gaps:         0

US-09-966-880A-8 (1-198) x US-09-326-186B-69 (1-20)

QY      176 LeuArgArgIleLeu 180
Db      1 CTGCGCCGATCCTG 15

RESULT 185
US-09-326-186B-166
; Sequence 166, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
```

```
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPR-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-326-186B-166

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:              4           Gaps:         0

US-09-966-880A-8 (1-198) x US-09-326-186B-166 (1-20)

QY      176 LeuArgArgIleLeu 180
Db      2 CTGCGCCGATCCTG 16

RESULT 186
US-08-750-088A-31
; Sequence 31, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: CDNA
US-08-750-088A-31

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-750-088A-31 (1-20)

Qy 92 ArgHisValAlaasp 96
Db 4 CGGCATGTCGGGAT 18

RESULT 187
US-09-502-344-59
; Sequence 59, Application US/09502344
; Patent No. 6331398
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/502,344
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/143,190
; FILING DATE: August 27, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-502-344-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-502-344-59 (1-20)

Qy 32 ValVallysargArg 36
Db 4 GTTGTAACGACGG 18

RESULT 188
US-09-712-266-67
; Sequence 67, Application US/09712266
; Patent No. 633158
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; TITLE OF INVENTION: SATO, Yoshihimi
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUKAI, Hiroyuki
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/712,266
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/446,504
; FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-712-266-67

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-712-266-67 (1-20)

Qy 156 GluArgThrPhelys 160
Db 3 GAGAGAAGCTTCAAG 17

RESULT 189
US-09-658-687A-16
; Sequence 16, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/09/658,687A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-16

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-658-687A-16 (1-20)

QY 107 ArgilePheThrAla 111
Db 1 CGTATCTTCACAGCT 15

RESULT 190
US-09-462-261-4
; Sequence 4, Application US/09462261
; Patent No. 6391636
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Oligonucleotide
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jane Massey Licata, Esq.
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: Pentium
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/462,261
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6391636member 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; APPLICATION NUMBER: 08/888,982
; FILING DATE: July 7, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
```

```
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-462-261-4

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-462-261-4 (1-20)

QY 169 SerValArgLeuSer 173
Db 4 TCTGTAGGCTTCA 18

RESULT 191
US-09-506-073-93
; Sequence 93, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-506-073-93

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-506-073-93 (1-20)

QY 169 SerValArgLeuSer 173
Db 4 TCTGTAGGCTTCA 18

RESULT 192
US-09-907-843-48/c
; Sequence 48, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
```

; CURRENT APPLICATION NUMBER: US/09/907,843  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 48  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-907-843-48

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-907-843-48 (1-20)

Qy 130 HisArgAlaGlyVal 134  
Db 20 CACCGGCGAGGTGA 6

RESULT 193  
US-09-676-610B-5  
; Sequence 5, Application US/09676610B  
; Patent No. 644465  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION  
; FILE REFERENCE: RTS-0138  
; CURRENT APPLICATION NUMBER: US/09/676,610B  
; CURRENT FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 182  
; SEQ ID NO 5  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-676-610B-5

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-676-610B-5 (1-20)

Qy 129 LeuHisArgAlaGly 133  
Db 6 TTGCACAGGCGCAGG 20

RESULT 194  
US-09-746-694-35  
; Sequence 35, Application US/09746694  
; Patent No. 6451538  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowbert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHK2 EXPRESSION  
; FILE REFERENCE: RTS-0228  
; CURRENT APPLICATION NUMBER: US/09/746,694  
; CURRENT FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 35  
; LENGTH: 20

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-746-694-35

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-746-694-35 (1-20)

Qy 110 ThrAlaArgLeuTyr 114  
Db 4 ACAGCAGGTTATAC 18

RESULT 195  
US-09-920-672-58  
; Sequence 58, Application US/09920672  
; Patent No. 6455308  
; GENERAL INFORMATION:  
; APPLICANT: Mark J. Graham  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION  
; FILE REFERENCE: RTS-0251  
; CURRENT APPLICATION NUMBER: US/09/920,672  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-920-672-58

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-920-672-58 (1-20)

Qy 42 PheSerLeuAspPhe 46  
Db 3 TTCTCGTTGGACTTC 17

RESULT 196  
US-09-657-453A-71/C  
; Sequence 71, Application US/09657453A  
; Patent No. 6458591  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 2 EXPRES

; FILE REFERENCE: RTS-0136  
; CURRENT APPLICATION NUMBER: US/09/657,453A  
; CURRENT FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 105  
; SEQ ID NO 71  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-657-453A-71

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-657-453A-71 (1-20)

Qy 38 SerAlaThrSerPhe 42

Db 15 TCTGCCACTTCTTTT 1

RESULT 197

US-09-153-242-56

; Sequence 56, Application US/09153242

; Patent No. 6482592

; GENERAL INFORMATION:

; APPLICANT: Lundberg, Joakim

; APPLICANT: Uhlen, Mathias

; TITLE OF INVENTION: MODULAR PROBES II

; FILE REFERENCE: 1181-242

; CURRENT APPLICATION NUMBER: US/09/153,242

; CURRENT FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: PCT/GB97/02629

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 56

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: KTH USP

US-09-153-242-56

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-153-242-56 (1-20)

Qy 32 ValValLysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 198

US-09-668-313A-78/c

; Sequence 78, Application US/09668313A

; Patent No. 6503756

; GENERAL INFORMATION:

; APPLICANT: Brett P. Moria

; APPLICANT: Susan M. Freier

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0127

; CURRENT APPLICATION NUMBER: US/09/668,313A

; CURRENT FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 247

; SEQ ID NO 78

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-668-313A-78

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-668-313A-78 (1-20)

Qy 44 LeuAspPheGlyTyr 48

Db 17 CTGGACTTTGGGTAT 3

RESULT 199

US-09-198-452A-3206/c

; Sequence 3206, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Grifffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3206

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3206

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-3206 (1-20)

Qy 169 SerValArgLeuSer 173

Db 19 TCCGTGAGACTGTCT 5

RESULT 200

US-09-198-452A-3704/c

; Sequence 3704, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Grifffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3704

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3704

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0



US-09-966-880A-8 (1-198) x US-09-198-452A-3704 (1-20)

QY 103 AsnLeuSerLeuArg 107  
Db 20 AACCTCTCTGAGG 6

## RESULT 201

US-09-198-452A-3731/C

; Sequence 3731, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3731

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3731

## Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-3731 (1-20)

QY 104 LeuSerLeuArgIle 108

Db 16 TTGTCTCTGGAATC 2

## RESULT 202

US-09-198-452A-3975

; Sequence 3975, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3975

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3975

## Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-3975 (1-20)

QY 176 LeuArgIleLeu 180

Db 6 TTGAGGAGGATCCTG 20

## RESULT 203

US-09-198-452A-4543

; Sequence 4543, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4543

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4543

## Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-4543 (1-20)

QY 111 AlaArgLeuTyrPhe 115

Db 2 GCCAGGCTGTATTC 16

## RESULT 204

US-09-198-452A-4632/C

; Sequence 4632, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4632

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4632

## Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-4632 (1-20)

QY 179 IleLeuLeuProLeu 183

Db 20 ATTCTACTCCCTCTC 6

## RESULT 205

US-09-198-452A-4660/C

; Sequence 4660, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

```
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4660
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4660

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             4            Gaps:          0

US-09-966-880A-8 (1-198) x US-09-198-452A-4660 (1-20)
QY      40 ThrSerPheSerLeu 44
        |||||
        18 ACATCGTCTCCCTA 4
Db

RESULT 206
US-09-198-452A-5412/c
; Sequence 5412, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5412
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5412

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             4            Gaps:          0

US-09-966-880A-8 (1-198) x US-09-198-452A-5412 (1-20)
QY      126 LeuArgArgLeuHis 130
        |||||
        17 CTAAGCGCTTACAT 3
Db

RESULT 207
US-09-198-452A-5709/c
; Sequence 5709, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5709
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5709

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             4            Gaps:          0

US-09-966-880A-8 (1-198) x US-09-198-452A-5709 (1-20)
QY      104 LeuSerLeuArgIle 108
        |||||
        15 CTGTCTCTCCGATA 1
Db

RESULT 208
US-09-198-452A-6382/c
; Sequence 6382, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6382
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6382

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             4            Gaps:          0

US-09-966-880A-8 (1-198) x US-09-198-452A-6382 (1-20)
QY      58 GluLeuLeuPheLeu 62
        |||||
        20 GAGCTTCTCTTTTA 6
Db

RESULT 209
US-09-198-452A-6501
; Sequence 6501, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6501

Alignment Scores:
Pred. No.:      1.11e+03      Length:      20
```

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-6501 (1-20)

QY 41 SerPheSerLeuAsp 45  
DB 5 AGTTTCTCTAGAC 19

## RESULT 210

US-09-843-376-54  
; Sequence 54, Application US/09843376  
; Patent No. 6566132  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 1 EXPRESSION  
; FILE REFERENCE: RTS-0234  
; CURRENT APPLICATION NUMBER: US/09/843,376  
; CURRENT FILING DATE: 2001-04-26  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 54  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-843-376-54

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-843-376-54 (1-20)

QY 167 GluAsnSerValArg 171  
DB 5 GAGATTTCAGTCAGG 19

## RESULT 211

US-09-909-595-70/c  
; Sequence 70, Application US/09909595  
; Patent No. 6586245  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Jacqueline Wyatt  
; APPLICANT: Scott E. Davis  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION  
; FILE REFERENCE: RTS-0223  
; CURRENT APPLICATION NUMBER: US/09/909,595  
; CURRENT FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 70  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-909-595-70

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-909-595-70 (1-20)

QY 2 AspSerLeuMet 6  
DB 15 GACAGTCTTCTCATG 1

## RESULT 212

US-09-972-115A-26  
; Sequence 26, Application US/09972115A  
; Patent No. 6599728  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Gregg, Morin B.  
; APPLICANT: Walter, Funk D.  
; APPLICANT: Mieczyslaw, Piatyszek A.  
; TITLE OF INVENTION: A Second Mammalian Telomerase  
; FILE REFERENCE: 080/003C  
; CURRENT APPLICATION NUMBER: US/09/972,115A  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US 60/128,577  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/129,123  
; PRIOR FILING DATE: 1999-04-13  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 26  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-972-115A-26

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-972-115A-26 (1-20)

QY 25 ArgGluThrTyrLeu 29  
DB 5 CGAGAGACTTATCTC 19

## RESULT 213

US-09-276-438-16  
; Sequence 16, Application US/09276438  
; Patent No. 6600027  
; GENERAL INFORMATION:  
; APPLICANT: Krishnan, Rajendra  
; APPLICANT: Coleman, Rebecca A.  
; APPLICANT: Yoder, Christine C.  
; APPLICANT: Durtschi, Becky A.  
; APPLICANT: Brake, David  
; TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULES ENCODING NEOSPORA PROTEINS  
; FILE REFERENCE: PC9943A  
; CURRENT APPLICATION NUMBER: US/09/276,438  
; CURRENT FILING DATE: 1999-03-25  
; EARLIER APPLICATION NUMBER: 60/079,389  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 60/112,282  
; EARLIER FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in Ver. 2.0 - beta  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA

; FILE REFERENCE: 4503/1G031

1. TITLE OF INVENTION

; TITLE OF INVENTION

/ NUMBER OF SEQUENCES: 30  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness  
/ STREET: 1420 Fifth Avenue  
/ CITY: Seattle  
/ STATE: WA  
/ COUNTRY: USA  
/ ZIP: 98101-8100  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/10261A  
/ FILING DATE: 02-SEP-1994  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Shelton, Dennis K.  
/ REGISTRATION NUMBER: 26,997  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 682-8100  
/ TELEFAX: (206) 224-0779  
/ INFORMATION FOR SEQ ID NO: 20:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 20 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA to mRNA  
/ DESCRIPTION: PCR primer; see TABLE 1  
/ HYPOTHETICAL: NO  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens  
/ PCT-US94-10261A-20

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-10261A-20 (1-20)

Cy 59 LeuLeuPheLeuArg 63  
Db 19 TTGCTATTCTCAGA 5

RESULT 218  
PCT-US95-08604-20  
; Sequence 20, Application PC/TUS9508604  
; GENERAL INFORMATION:  
; APPLICANT: Visible Genetics Inc.  
; APPLICANT: HSC Research and Development Limited Partnership  
; APPLICANT: Gallie, Brenda L.  
; APPLICANT: Dunn, James M.  
; APPLICANT: Stevens, John K.  
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis  
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Opedahl & Larson  
; STREET: 1992 Commerce Street, Suite 309  
; CITY: Yorktown Heights  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10598-4412  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0

/ SOFTWARE: Word Perfect  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US95/08604  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION NUMBER: US 08/271,942  
/ FILING DATE: 08-JUL-1994  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Marina T. Larson  
/ REGISTRATION NUMBER: 32,038  
/ REFERENCE/DOCKET NUMBER: VGEN.P-003-WO  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (914) 245-3252  
/ TELEFAX: (914) 962-4330  
/ TELEX:  
/ INFORMATION FOR SEQ ID NO: 20:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 20  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: genomic DNA  
/ HYPOTHETICAL: no  
/ ANTI-SENSE: no  
/ FRAGMENT TYPE: internal  
/ ORIGINAL SOURCE:  
/ ORGANISM: human  
/ FEATURE:  
/ NAME/KEY: primer for exon 21 of human RB1 gene  
/ PCT-US95-08604-20

Alignment Scores:  
Pred. No.: 1.11e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US95-08604-20 (1-20)

Cy 28 TyrLeuCysTyrVal 32  
Db 2 TACCTATGTATGTT 16

RESULT 219  
PCT-US95-08606-20  
; Sequence 20, Application PC/TUS9508606  
; GENERAL INFORMATION:  
; APPLICANT: Visible Genetics Inc.  
; APPLICANT: Stevens, John K.  
; APPLICANT: Dunn, James M.  
; APPLICANT: Capatos, Denis  
; APPLICANT: Matthews, David E.  
; TITLE OF INVENTION: Method for Testing for Mutations in DNA  
; TITLE OF INVENTION: from a Patient Sample  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Opedahl & Larson  
; STREET: 1992 Commerce Street, Suite 309  
; CITY: Yorktown Heights  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10598-4412  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08606  
; FILING DATE:

```
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: US 08/271,946
/ APPLICATION NUMBER: 08-JUL-1994
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marina T. Larson
/ REGISTRATION NUMBER: 32,038
/ REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (914) 245-3252
/ TELEFAX: (914) 962-4330
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ HYPOTHEICAL: no
/ ANTI-SENSE: no
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: human
/ FEATURE:
/ NAME/KEY: primer for exon 21 of human Rb1 gene
PCT-US95-08606-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US95-08606-20 (1-20)

QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16

RESULT 220
US-07-974-447-16
; Sequence 16, Application US/07974447
; Patent No. 5436142
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H
; APPLICANT: Libitsyn, Nikolai
; TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO GENOMIC
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/974,447
; FILING DATE: 12-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-57438/BIR CSHL-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 3983249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-149-199-16
```

```
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
US-07-974-447-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-974-447-16 (1-12)

QY 41 SerPheSerLeu 44
Db 1 AGCTTCTCCTC 12

RESULT 221
US-08-149-199-16
; Sequence 16, Application US/08149199
; Patent No. 5501964
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H
; APPLICANT: Libitsyn, Nikolai
; TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO GENOMIC
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 941114187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,199
; FILING DATE: 9-No. 5501964-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A57438/BIR CSHL002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 7811989
; TELEFAX: (415) 3983249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-149-199-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-149-199-16 (1-12)

QY 41 SerPheSerLeu 44  
DB 1 AGCTTCTCCCTC 12

RESULT 222  
US-08-757-024-852/c  
; Sequence 852, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 852:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-852

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-852 (1-12)

QY 90 CysalaArgHis 93  
DB 12 TGTGCCCGCCAT 1

RESULT 223  
US-09-115-061-16  
; Sequence 16, Application US/09115061A  
; Patent No. 6159713  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael  
; APPLICANT: Lisitsyn, Nikolai  
; TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS

; FILE REFERENCE: CSHL.002.03US  
; CURRENT APPLICATION NUMBER: US/09/115,061A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: 08/478,342  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/149,199  
; EARLIER FILING DATE: 1993-11-09  
; EARLIER APPLICATION NUMBER: 07/974,447  
; EARLIER FILING DATE: 1992-11-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: OLIGONUCLEOTIDE  
US-09-115-061-16

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-115-061-16 (1-12)

QY 41 SerPheSerLeu 44  
DB 1 AGCTTCTCCCTC 12

RESULT 224  
US-09-049-190-15/c  
; Sequence 15, Application US/09049190  
; Patent No. 6190866  
; GENERAL INFORMATION:  
; APPLICANT: Nielsen et al.  
; TITLE OF INVENTION: Peptide Nucleic Acids Having  
; TITLE OF INVENTION: Antibacterial Activity  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,190  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: John W. Caldwell  
; REGISTRATION NUMBER: 28,937  
; REFERENCE/DOCKET NUMBER: ISIS-2560  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 bases  
; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
; OTHER INFORMATION: backbone
; US-09-049-190-15

```

```

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-049-190-15 (1-12)

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```

Qy 119 ArgLysAlaGlu 122
Db 12 AGAAGGCAGAA 1

RESULT 225
US-08-098-327E-39/c
; Sequence 39, Application US/08098327E
; Patent No. 6270771
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,327E
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; US-08-098-327E-39

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-098-327E-39 (1-12)

Qy 59 LeuLeuPheLeu 62
Db 12 TTGTTGTTCTTG 1

RESULT 226
US-08-098-327E-43/c
; Sequence 43, Application US/08098327E
; Patent No. 6270771
; GENERAL INFORMATION:

```



APPLICANT: GUERIN-MARCHAND, Claudine  
APPLICANT: DRUILHE, Pierre  
TITLE OF INVENTION: PETIDE SEQUENCES SPECIFIC FOR THE  
TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/098,327E  
FILING DATE: 24-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 01286  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 010830-045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 92/13884  
PUBLICATION DATE: 20-AUG-1992  
US-08-098-327E-43

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-098-327E-43 (1-12)

QY 59 LeuLeuPheLeu 62  
Db 12 TTGTTGTTCTTG 1

RESULT 227  
US-09-261-079-16  
Sequence 16, Application US/09261079  
Patent No. 6277606  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael  
APPLICANT: Lisitsyn, Nikolai  
TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS  
FILE REFERENCE: CSHL.002.04US  
CURRENT APPLICATION NUMBER: US/09/261,079  
CURRENT FILING DATE: 1999-03-02  
EARLIER APPLICATION NUMBER: 08/478,242  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 07/974,447  
EARLIER FILING DATE: 1992-11-12

APPLICANT: GUERIN-MARCHAND, Claudine  
APPLICANT: DRUILHE, Pierre  
TITLE OF INVENTION: PETIDE SEQUENCES SPECIFIC FOR THE  
TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/098,327E  
FILING DATE: 24-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 01286  
FILING DATE: 05-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm K.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 010830-045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 92/13884  
PUBLICATION DATE: 20-AUG-1992  
US-08-098-327E-43

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-261-079-16 (1-12)

QY 41 SerPheSerLeu 44  
Db 1 AGCTTCTCCCTC 12

RESULT 228  
US-08-932-140C-15/c  
Sequence 15, Application US/08932-140C  
Patent No. 6300318  
GENERAL INFORMATION:  
APPLICANT: Nielsen et al.  
TITLE OF INVENTION: Peptide Nucleic Acids Having  
TITLE OF INVENTION: Antibacterial Activity  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: No. 6300318ris LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/932,140C  
FILING DATE: September 16, 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Caldwell  
REGISTRATION NUMBER: 28,937  
REFERENCE/DOCKET NUMBER: ISIS-2560  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:

NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-  
OTHER INFORMATION: lysine-glycine backbone  
US-08-932-140C-15

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-932-140C-15 (1-12)

QY 119 ArgIyeAlaqlu 122  
DB 12 AGAAGGCAGAA 1

RESULT 229

US-08-462-625-39/c

; Sequence 39, Application US/08462625

; Patent No. 6319502  
; GENERAL INFORMATION:  
; APPLICANT: GUERIN-MARCHAND, Claudine  
; APPLICANT: DRUILHE, Pierre  
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE  
; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE  
; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,625  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/038,327  
; FILING DATE: 24-NOV-1993  
; PRIOR APPLICATION DATA: FR 91 01286  
; FILING DATE: 05-FEB-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McGowan, Malcolm K.  
; REGISTRATION NUMBER: 39,300  
; REFERENCE/DOCKET NUMBER: 010830-078  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; PUBLICATION INFORMATION:  
; DOCUMENT NUMBER: WO 92/13884  
; PUBLICATION DATE: 20-AUG-1992  
; US-08-462-625-39

Alignment Scores:  
Pred. No.: 7.75e+03 Length: 12  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-462-625-39 (1-12)

QY 59 LeuLeuPheLeu 62  
DB 12 TTGTTGTTCTTG 1

RESULT 230

US-08-462-625-43/c

; Sequence 43, Application US/08462625

; Patent No. 6319502

; GENERAL INFORMATION:

; APPLICANT: GUERIN-MARCHAND, Claudine

; APPLICANT: DRUILHE, Pierre

; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE

; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE

; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES

```

; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,625
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/098,327
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
;
; US-08-462-625-43
;
; Alignment Scores:
; Pred. No.: 7.75e+03 Length: 12
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 4 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-462-625-43 (1-12)
;
; QY 59 LeuLeuPheLeu 62
; Db 12 TTGTTGTTCTTG 1
;
; RESULT 231
; US-08-173-489C-350/c
; Sequence 350, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 350:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from p53 gene
; DESCRIPTION: region in Seq ID No. 5861244349
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 350 :FROM 1 TO 13
;
; US-08-173-489C-350
;
; Alignment Scores:
; Pred. No.: 8.38e+03 Length: 13
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 2 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-173-489C-350 (1-13)
;
; QY 22 LysGlyArgArg 25
; Db 13 AAAGGAAGGCGA 2
;
; RESULT 232
; US-08-757-024-840/c
; Sequence 840, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```

NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5218-41  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 840:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-024-840

Alignment Scores:  
Pred. No.: 8.38e+03 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-840 (1-13)

QY 90 CysalaargHis 93  
Db 13 TGTGCCGCCAT 2

RESULT 233  
US-08-757-024-851/c  
Sequence 851, Application US/08757024  
Patent No. 6025339  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
NUMBER OF SEQUENCES: 952  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
STREET: P.O. Drawer 34009  
CITY: Charlotte  
STATE: No. 6025339th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,024  
FILING DATE: 26-NOV-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5218-41  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 851:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-024-851

Alignment Scores:  
Pred. No.: 8.38e+03 Length: 13

Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-851 (1-13)

QY 90 CysalaargHis 93  
Db 12 TGTGCCGCCAT 1

RESULT 234  
US-08-981-988A-39/c  
Sequence 39, Application US/08981988A  
Patent No. 6337194  
GENERAL INFORMATION:  
APPLICANT: Vittal Mallya Scientific Research Foundation  
APPLICANT: The University of Leicester  
TITLE OF INVENTION: Insulin  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: VITTAL MALLYA SCIENTIFIC RESEARCH FOUNDATION  
STREET: K. R. ROAD  
CITY: BANGALORE  
COUNTRY: INDIA  
ZIP: 560 004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,988A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9513967.1  
FILING DATE: 08-JUL-1995  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-981-988A-39

Alignment Scores:  
Pred. No.: 8.38e+03 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-981-988A-39 (1-13)

QY 41 SerPheSerLeu 44  
Db 12 AGCTTCAGCCTC 1

RESULT 235  
US-08-532-657A-3/c  
Sequence 3, Application US/08532657A  
Patent No. 6346414  
GENERAL INFORMATION:  
APPLICANT: JACOBS, Eric  
TITLE OF INVENTION: TRANSPOSITION ASSEMBLY FOR GENE TRANSFER  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404

CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,657A  
FILING DATE: 16-OCT-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR94/00419  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93/04530  
FILING DATE: 16-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rea, Teresa Stanek  
REGISTRATION NUMBER: 30,427  
REFERENCE/DOCKET NUMBER: 017753-069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: synthetic oligonucleotide  
US-08-532-657A-3

Alignment Scores:  
Pred. No.: 13  
Score: 8.38e+03  
Matches: 4  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-532-657A-3 (1-13)

Qy 46 PheGlyTyrLeu 49  
|||||  
Db 13 TTGCGTACCTT 2

RESULT 236  
US-09-323-872A-58/c  
Sequence 58, Application US/09323872A  
Patent No. 6395539  
GENERAL INFORMATION:  
APPLICANT: Coschigano, Peter  
TITLE OF INVENTION: Compositions and Methods for Bioremediation  
FILE REFERENCE: CHU-03640  
CURRENT APPLICATION NUMBER: US/09/323,872A  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 09/072,433  
PRIOR FILING DATE: 1998-05-04  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 58  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-323-872A-58

Alignment Scores:  
Pred. No.: 13  
Score: 8.38e+03  
Matches: 4  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-323-872A-58 (1-13)

Qy 195 ThrLeuGlyLeu 198  
|||||  
Db 13 ACACAGGGCTG 2

RESULT 237  
US-08-275-951-65  
Sequence 65, Application US/08275951  
Patent No. 6451968  
GENERAL INFORMATION:  
APPLICANT: Egholm, Michael  
APPLICANT: Kiely, John  
APPLICANT: Griffin, Michael  
APPLICANT: Coull, James M.  
APPLICANT: Neilsen, Peter  
APPLICANT: Buchardt, Ole  
APPLICANT: Dueholm, Kim L.  
APPLICANT: Christensen, Leif  
TITLE OF INVENTION: Linked Peptide Nucleic Acids  
FILE REFERENCE: ISIS1577  
CURRENT APPLICATION NUMBER: US/08/275,951  
CURRENT FILING DATE: 1994-07-15  
PRIOR APPLICATION NUMBER: 08/108,591  
PRIOR FILING DATE: 1993-11-22  
PRIOR APPLICATION NUMBER: 08/088,658  
PRIOR FILING DATE: 1993-07-02  
PRIOR APPLICATION NUMBER: 08/088,661  
PRIOR FILING DATE: 1993-07-02  
PRIOR APPLICATION NUMBER: PCT/EP92/01219  
PRIOR FILING DATE: 1992-05-22  
PRIOR APPLICATION NUMBER: 986/91  
PRIOR FILING DATE: 1991-05-22  
PRIOR APPLICATION NUMBER: 987/91  
PRIOR FILING DATE: 1991-05-24  
PRIOR APPLICATION NUMBER: 510/92  
PRIOR FILING DATE: 1991-04-15  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 65  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence  
US-08-275-951-65

Alignment Scores:  
Pred. No.: 13  
Score: 8.38e+03  
Matches: 4  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 2.02%  
Indels: 0  
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-275-951-65 (1-13)

Qy 24 ArgArgGluThr 27  
|||||  
Db 1 CGCAGAGAACG 12

RESULT 238  
US-09-216-584-1  
Sequence 1, Application US/09216584  
Patent No. 6548657

```

; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Beillon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-1

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0

US-09-966-880A-8 (1-198) x US-09-216-584-1 (1-13)

Qy  59 LeuLeuPheLeu 62
    |||||
Db  1 TTGCTTTTCCTC 12

RESULT 239
US-09-216-584-2
; Sequence 2, Application US/09216584
; Patent No. 6548657
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Beillon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-2

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0

```

```

Query Match:    2.02%        0
DB:             4            0

US-09-966-880A-8 (1-198) x US-09-216-584-2 (1-13)

Qy  59 LeuLeuPheLeu 62
    |||||
Db  2 TTGCTTTTCCTC 13

RESULT 240
US-09-216-584-13
; Sequence 13, Application US/09216584
; Patent No. 6548657
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Beillon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-13

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0

US-09-966-880A-8 (1-198) x US-09-216-584-13 (1-13)

Qy  70 LeuAspProGly 73
    |||||
Db  1 CTGGATCCAGGA 12

RESULT 241
US-09-083-235A-74
; Sequence 74, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haalma, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence  
US-09-083-235A-74

Alignment Scores:  
Pred. No.: 8.38e+03 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-083-235A-74 (1-13)

Qy 24 ArgArgGluThr 27  
Db 1 CGCAGAGAGACG 12

RESULT 242  
US-09-083-235A-78  
Sequence 78, Application US/09083235A  
Patent No. 6632919  
GENERAL INFORMATION:  
APPLICANT: Nielsen, Peter E  
APPLICANT: Haaima, Gerald  
APPLICANT: Eldrup, Anne B  
TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers  
FILE REFERENCE: ISIS3044  
CURRENT APPLICATION NUMBER: US/09/083,235A  
CURRENT FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 08/862,629  
PRIOR FILING DATE: 1997-05-23  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 78  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence  
US-09-083-235A-78

Alignment Scores:  
Pred. No.: 8.38e+03 Length: 13  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-083-235A-78 (1-13)

Qy 24 ArgArgGluThr 27  
Db 1 CGCAGAGAGACG 12

RESULT 243  
US-08-375-116A-122/c  
Sequence 122, Application US/08375116A  
Patent No. 5631146  
GENERAL INFORMATION:  
APPLICANT: Szostak, Jack W.  
APPLICANT: Huizenga, David E.  
TITLE OF INVENTION: DNA APTAMERS AND CATALYSTS THAT BIND  
TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE-5'-PHOSPHATES AND METHODS FOR  
ISOLATION THEREOF  
NUMBER OF SEQUENCES: 136  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,116A  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/266001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (9617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-375-116A-122

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-375-116A-122 (1-14)

Qy 61 PheLeuArgTyr 64  
Db 12 TTCCTCCGCTAT 1

RESULT 244  
US-08-320-559-16/c  
Sequence 16, Application US/08320559  
Patent No. 5633135  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo  
APPLICANT: Ganaani, Eli  
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for  
Detection and Treatment of Acute Leukemias  
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the  
TITLE OF INVENTION: All-1 Region  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,559  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/062,443  
FILING DATE: 14 MAY 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,094  
FILING DATE: 30-OCT-92

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/888,830  
;; FILING DATE: 27-MAY-92  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/805,093  
;; FILING DATE: 11-DEC-91  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Deluca, Mark  
;; REGISTRATION NUMBER: 33,229  
;; REFERENCE/DOCKET NUMBER: TJU-0855  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568-3439  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; ANTI-SENSE: No  
US-08-320-559-16

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-320-559-16 (1-14)  
QY 46 PheGlyTyrLeu 49  
DB 13 TTGGGTACCT 2

RESULT 245  
US-08-327-392-16/c  
; Sequence 16, Application US/08327392  
; Patent No. 5633136  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo  
; APPLICANT: Canaan, Eli  
; TITLE OF INVENTION: ALL-1 Polynucleotides and Monoclonal  
; TITLE OF INVENTION: Antibodies for Leukemia Detection and  
; TITLE OF INVENTION: Treatment  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633136ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/327,392  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/971,094  
; FILING DATE: 30-OCT-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/888,830  
; FILING DATE: 27-MAY-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,093  
; FILING DATE: 11-DEC-91  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Deluca, Mark  
;; REGISTRATION NUMBER: 33,229  
;; REFERENCE/DOCKET NUMBER: TJU-1331  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568-3439  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; ANTI-SENSE: No  
US-08-327-392-16

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-327-392-16 (1-14)  
QY 46 PheGlyTyrLeu 49  
DB 13 TTGGGTACCT 2

RESULT 246  
US-08-486-421-42  
; Sequence 42, Application US/08486421  
; Patent No. 5672479  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,421  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470,911  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-486-421-42



Alignment Scores: 9.02e+03 Length: 14  
Pred. No.: 4.00 Matches: 4  
Score: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-486-421-42 (1-14)  
QY 126 LeuArgArgLeu 129  
DB 3 CTTGCCGCCCTC 14  
RESULT 247  
US-08-135-809A-5/c  
; Sequence 5, Application US/08135809A  
; Patent No. 5688677  
; GENERAL INFORMATION:  
; APPLICANT: CHENG, SENG H.  
; APPLICANT: DITULLIO, PAUL  
; APPLICANT: EBERT, KARL M.  
; APPLICANT: MEADE, HARRY M.  
; APPLICANT: SMITH, ALAN E.  
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS CONTAINING  
; TITLE OF INVENTION: INACTIVATED HORMONE RESPONSIVE ELEMENTS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: GENZYME CORPORATION  
; STREET: ONE MOUNTAIN ROAD  
; CITY: FRAMINGHAM  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 01701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/135,809A  
; FILING DATE: 13-OCT-1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LASSEN, ELIZABETH  
; REGISTRATION NUMBER: 31,845  
; REFERENCE/DOCKET NUMBER: IG4-9.12  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 872-8400  
; TELEFAX: (508) 872-5415  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-135-809A-5  
Alignment Scores: 9.02e+03 Length: 14  
Pred. No.: 4.00 Matches: 4  
Score: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-135-809A-5 (1-14)  
QY 2 AppSerLeuLeu 5  
DB 12 GACAGCCTCTC 1

RESULT 248  
US-08-271-880A-210/c  
; Sequence 210, Application US/08271880A  
; Patent No. 5693535  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; APPLICANT: Bharat Chowrira  
; APPLICANT: James McSwiggen  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/271,880A  
; FILING DATE: July 7, 1994  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/103,243  
; FILING DATE: August 6, 1993  
; APPLICATION NUMBER: 07/882,886  
; FILING DATE: May 14, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 206/116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 210:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-271-880A-210  
Alignment Scores: 9.02e+03 Length: 14  
Pred. No.: 4.00 Matches: 4  
Score: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0  
US-09-966-880A-8 (1-198) x US-08-271-880A-210 (1-14)  
QY 10 LysPheLeuTyr 13  
DB 12 AAGTTCTCTAT 1  
RESULT 249  
US-08-271-880A-211/c  
; Sequence 211, Application US/08271880A  
; Patent No. 5693535

```

; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.880A
; FILING DATE: July 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-880A-211
; Alignment Scores:
; Pred. No.: 9.02e+03 Length: 14
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 1 Gaps: 0
; US-09-966-880A-8 (1-198) x US-08-271-880A-211 (1-14)
;
; Qy 11 PheLeuTyxGln 14
; Db 12 TTTCTCTATCAA 1
;
; RESULT 250
; US-08-470-911-42
; Sequence 42, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-470-911-42
; Alignment Scores:
; Pred. No.: 9.02e+03 Length: 14
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 1 Gaps: 0
; US-09-966-880A-8 (1-198) x US-08-470-911-42 (1-14)
;
; Qy 126 LeuArgArgLeu 129
; Db 3 CTTTCGGCGCTC 14
;
; RESULT 251
; US-08-323-192D-66/c
; Sequence 66, Application US/08323192D
; Patent No. 5785199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

```
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-323-192D-66

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-323-192D-66 (1-14)

Qy 59 LeuLeupheLeu 62
Db 14 CTCCTGTTTCTA 3

RESULT 252
US-08-470-887A-54/c
Sequence 54, Application US/08470887A
Patent No. 5820871
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,887A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA
US-08-470-887A-54

Qy 59 LeuLeupheLeu 62
Db 14 CTCCTGTTTCTA 3

RESULT 254
US-08-470-887A-54
```

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Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-470-887A-54 (1-14)

Qy 59 LeuLeupheLeu 62
Db 14 CTCCTGTTTCTA 3

RESULT 253
US-08-252-508B-54/c
Sequence 54, Application US/08252508B
Patent No. 5854037
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,508B
FILING DATE: 01-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA
US-08-252-508B-54

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-252-508B-54 (1-14)

Qy 59 LeuLeupheLeu 62
Db 14 CTCCTGTTTCTA 3

RESULT 254
US-08-486-809-42
```

; Sequence 42, Application US/08486809  
; Patent No. 5869622  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,809  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470,911  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-053  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-486-809-42  
  
Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-08-486-809-42 (1-14)  
  
Qy 126 LeuArgLeu 129  
Db 3 CTTGCGCGCTC 14  
  
RESULT 255  
US-08-910-408-210/c  
; Sequence 210, Application US/08910408  
; Patent No. 5972704  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; APPLICANT: Bharat Chowrira  
; APPLICANT: James McSwiggen  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA: US/08/910,408  
; APPLICATION NUMBER: US/08/910,408  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/271,880  
; FILING DATE: July 7, 1994  
; APPLICATION NUMBER: 08/103,243  
; FILING DATE: August 6, 1993  
; APPLICATION NUMBER: 07/882,886  
; FILING DATE: May 14, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 206/116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 210:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-910-408-210  
  
Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x US-08-910-408-210 (1-14)  
  
Qy 10 LysPheLeuTyr 13  
Db 12 AAGTTTCTCTAT 1  
  
RESULT 256  
US-08-910-408-211/c  
; Sequence 211, Application US/08910408  
; Patent No. 5972704  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth G. Draper  
; APPLICANT: Bharat Chowrira  
; APPLICANT: James McSwiggen  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

```

; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,880
; FILING DATE: July 7, 1994
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-910-408-211

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-910-408-211 (1-14)

Qy 11 PheLeuTyGln 14
Db 12 TTTCCTATCAA 1

RESULT 257
US-08-520-933-4
; Sequence 4, Application US/08520933
; Patent No. 5981194
; GENERAL INFORMATION:
; APPLICANT: Jefferies, Wilfred A.
; APPLICANT: McGeer, Patrick L.
; APPLICANT: Rothernberger, Sylvia
; APPLICANT: Food, Michael R.
; APPLICANT: Yamada, Tatsuo
; APPLICANT: Kennard, Malcolm
; TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
; TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,933
; FILING DATE: August 31, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Shona S. McDiarmid
; REGISTRATION NUMBER: 38,798
; REFERENCE/DOCKET NUMBER: 7685-006
; TELEPHONE: 416-364-7311
; TELEFAX: 416-361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-520-933-4

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-520-933-4 (1-14)

Qy 95 AlaAspPheLeu 98
Db 1 GCGGACTTCCTC 12

RESULT 258
US-09-106-377-54/c
; Sequence 54, Application US/09106377
; Patent No. 6001634
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

```

; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: RNA  
US-09-106-377-54

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-106-377-54 (1-14)

Oy 59 LeuLeupheLeu 62  
Db 14 CTCCTGTTCTCA 3

RESULT 259  
US-08-757-024-827/c  
; Sequence 827, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,024  
FILING DATE: 26-NOV-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5218-41  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 827:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-024-827

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-08-757-024-827  
; Sequence 827, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-827 (1-14)

Oy 90 CysAlaArgHis 93  
Db 14 TGTGCCGCCAT 3  
RESULT 260  
US-08-757-024-839/c  
; Sequence 839, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,024  
FILING DATE: 26-NOV-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5218-41  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 839:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-024-839

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-839 (1-14)

Oy 90 CysAlaArgHis 93  
Db 13 TGTGCCGCCAT 2

RESULT 261  
US-08-757-024-850/c  
; Sequence 850, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina

```

; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 850:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-024-850

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-850 (1-14)

Qy 90 CysAlaArGHis 93
Db 12 TTGCGCCGCAT 1

RESULT 262
US-08-545-860D-16/c
; Sequence 16, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994

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; PRIOR APPLICATION DATA: PCT/US92/10930
; APPLICATION NUMBER: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: No
; US-08-545-860D-16

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-545-860D-16 (1-14)

Qy 46 PheGlyTyrLeu 49
Db 13 TTGGGTACCTT 2

RESULT 263
US-08-985-162-1779/c
; Sequence 1779, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,162  
 FILING DATE: 04 December 1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/036,476  
 FILING DATE: 31 January 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/107  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1779:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-985-162-1779

Alignment Scores:  
 Pred. No.: 9.02e+03 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-985-162-1779 (1-14)

Qy 130 HisaGAlagly 133  
 Db 13 CACAGGCGAGG 2

RESULT 264

US-08-985-162-1821  
 ; Sequence 1821, Application US/08985162  
 ; Patent No. 6057156  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akhtar, Saghir  
 ; APPLICANT: Fell, Patricia  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
 ; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
 ; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
 ; TITLE OF INVENTION: FACTOR RECEPTORS  
 ; NUMBER OF SEQUENCES: 1877  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/985,162  
 ; FILING DATE: 04 December 1997  
 ; CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/036,476  
 FILING DATE: 31 January 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/107  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 1821:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-985-162-1821

Alignment Scores:  
 Pred. No.: 9.02e+03 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-985-162-1821 (1-14)

Qy 134 ValGlnIleAla 137  
 Db 1 GUGCAGAUGC GA 12

RESULT 265

US-09-249-215-210/c  
 ; Sequence 210, Application US/09249215  
 ; Patent No. 6159692  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kenneth G. Draper  
 ; APPLICANT: Bharat Chowrira  
 ; APPLICANT: James McSwiggen  
 ; APPLICANT: Dan T. Stinchcomb  
 ; APPLICANT: James D. Thompson  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
 ; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS  
 ; TITLE OF INVENTION: REPLICATION  
 ; NUMBER OF SEQUENCES: 232  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/249,215  
 ; FILING DATE: 12-Feb-1999  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/910,408  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/103,243  
 ; FILING DATE: August 6, 1993  
 ; APPLICATION NUMBER: 07/882,886  
 ; FILING DATE: May 14, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard



REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 206/116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 210:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 210:  
US-09-249-215-210

Alignment Scores:  
Pred. No.: 14 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-249-215-210 (1-14)

QY 10 LysPheLeuTyr 13  
Db 12 AAGTTTCTCTAT 1

RESULT 266  
US-09-249-215-211/c  
Sequence 211, Application US/09249215  
Patent No. 6159692  
GENERAL INFORMATION:  
APPLICANT: Kenneth G. Draper  
James McSwiggen  
Bharat Chowrira  
Dan T. Stinchcomb  
James D. Thompson  
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING  
HUMAN IMMUNODEFICIENCY VIRUS  
REPLICATION  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,215  
FILING DATE: 12-Feb-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/910,408  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/103,243  
FILING DATE: August 6, 1993  
APPLICATION NUMBER: 07/882,886  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 206/116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 211:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 211:  
US-09-249-215-211

Alignment Scores:  
Pred. No.: 14 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-249-215-211 (1-14)

QY 11 PheLeuTyrGln 14  
Db 12 TTTTCTCTATCAA 1

RESULT 267  
US-09-156-828B-25/c  
Sequence 25, Application US/09156828B  
Patent No. 6238917  
GENERAL INFORMATION:  
APPLICANT: Hendry, Philip  
APPLICANT: McCall, Maxine J.  
TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZYMES  
FILE REFERENCE: 50534bpu  
CURRENT APPLICATION NUMBER: US/09/156,828B  
CURRENT FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: PCT/AU97/00210  
PRIOR FILING DATE: 1997-04-02  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 25  
LENGTH: 14  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and Portions thereof  
US-09-156-828B-25

Alignment Scores:  
Pred. No.: 14 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-156-828B-25 (1-14)

QY 95 AlaAspPheLeu 98  
Db 14 GCTGACTTCTGT 3

RESULT 268  
US-08-666-341A-75  
Sequence 75, Application US/08666341A  
Patent No. 6365345  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Antisense nucleic Acids for the  
prevention and treatment of disorders in which expression  
of c-erbB plays a role  
TITLE OF INVENTION: of c-erbB  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman and Stern, PLLC  
STREET: 400 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/666,341A  
FILING DATE: 15-AUG-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93120710.4  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-666-341A-75  
Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB: 0  
US-09-966-880A-8 (1-198) x US-08-666-341A-75 (1-14)  
QY 172 LeuSerArgGln 175  
Db 1 CTGTCGCTCAA 12  
RESULT 269  
US-09-285-040-4  
Sequence 4, Application US/09285040  
Patent No. 6455494  
GENERAL INFORMATION:  
APPLICANT: Jefferies, Wilfred A.  
APPLICANT: McGeer, Patrick L.  
APPLICANT: Rothenberger, Sylvia  
APPLICANT: Food, Michael R.  
APPLICANT: Yamada, Tatsuo  
APPLICANT: Kennard, Malcolm  
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins  
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bereekin & Parr  
STREET: 40 King Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/285,040  
FILING DATE: 01-APR-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gravelle, Micheline

REGISTRATION NUMBER: 40,261  
REFERENCE/DOCKET NUMBER: 7695-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 416-364-7311  
TELEFAX: 416-361-1398  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-09-285-040-4  
Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB: 0  
US-09-966-880A-8 (1-198) x US-09-285-040-4 (1-14)  
QY 95 AlaAspPheLeu 98  
Db 1 GCGGACTTCCTC 12  
RESULT 270  
US-09-516-277-14  
Sequence 14, Application US/09516277  
Patent No. 6528701  
GENERAL INFORMATION:  
APPLICANT: WANG -- OARD  
TITLE OF INVENTION: RICE UBQUITIN-DERIVED PROMOTERS  
FILE REFERENCE: 98A5  
CURRENT APPLICATION NUMBER: US/09/516,277  
CURRENT FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 14  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-516-277-14  
Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
Gaps: 0  
DB: 0  
US-09-966-880A-8 (1-198) x US-09-516-277-14 (1-14)  
QY 36 ArgAspSerAla 39  
Db 3 CGAGATTCGCT 14  
RESULT 271  
US-08-192-943-14/C  
Sequence 14, Application US/08192943  
Patent No. 6544755  
GENERAL INFORMATION:  
APPLICANT: James D. Thompson  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
TITLE OF INVENTION: BY EXPRESSION OF THE c-MYC  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 41